

PCT

WORLD INTELLECTUAL PROPERTY ORGANIZATION
International Bureau



INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(51) International Patent Classification 6 : C07K 14/00, A61K 39/00	A2	(11) International Publication Number: WO 98/37093
		(43) International Publication Date: 27 August 1998 (27.08.98)

(21) International Application Number: PCT/US98/03492	(81) Designated States: AL, AM, AT, AU, BA, BB, BG, BR, BY, CA, CH, CN, CU, CZ, DE, DK, EE, ES, FI, GB, GE, GH, GM, GW, HU, ID, IL, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD, SE, SG, SI, SK, SL, TJ, TM, TR, TT, UA, UG, UZ, VN, YU, ZW, ARIPO patent (GH, GM, KE, LS, MW, SD, SZ, UG, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, ML, MR, NE, SN, TD, TG).
(22) International Filing Date: 25 February 1998 (25.02.98)	
(30) Priority Data: 08/806,099 25 February 1997 (25.02.97) US 08/904,804 1 August 1997 (01.08.97) US 09/020,956 9 February 1998 (09.02.98) US	
(71) Applicant: CORIXA CORPORATION [US/US]; Suite 200, 1124 Columbia Street, Seattle, WA 98104 (US).	
(72) Inventors: XU, Jiangchun; 15805 Southeast 43rd Place, Bellevue, WA 98006 (US). DILLON, Davin, C.; 21607 N.E. 24th Street, Redmond, WA 98053 (US).	
(74) Agents: MAKI, David, J. et al.; Seed and Berry LLP, 6300 Columbia Center, 701 Fifth Avenue, Seattle, WA 98104-7092 (US).	

(54) Title: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER AND METHODS FOR THEIR USE

(57) Abstract

Compounds and methods for treating prostate cancer are provided. The inventive compounds include polypeptides containing at least a portion of a prostate tumor protein. Vaccines and pharmaceutical compositions for immunotherapy of prostate cancer comprising such polypeptides, or DNA molecules encoding such polypeptides, are also provided, together with DNA molecules for preparing the inventive polypeptides.

FOR THE PURPOSES OF INFORMATION ONLY

Codes used to identify States party to the PCT on the front pages of pamphlets publishing international applications under the PCT.

AL	Albania	ES	Spain	LS	Lesotho	SI	Slovenia
AM	Armenia	FI	Finland	LT	Lithuania	SK	Slovakia
AT	Austria	FR	France	LU	Luxembourg	SN	Senegal
AU	Australia	GA	Gabon	LV	Latvia	SZ	Swaziland
AZ	Azerbaijan	GB	United Kingdom	MC	Monaco	TD	Chad
BA	Bosnia and Herzegovina	GE	Georgia	MD	Republic of Moldova	TG	Togo
BB	Barbados	GH	Ghana	MG	Madagascar	TJ	Tajikistan
BE	Belgium	GN	Guinea	MK	The former Yugoslav Republic of Macedonia	TM	Turkmenistan
BF	Burkina Faso	GR	Greece	ML	Mali	TR	Turkey
BG	Bulgaria	HU	Hungary	MN	Mongolia	TT	Trinidad and Tobago
BJ	Benin	IE	Ireland	MR	Mauritania	UA	Ukraine
BR	Brazil	IL	Israel	MW	Malawi	UG	Uganda
BY	Belarus	IS	Iceland	MX	Mexico	US	United States of America
CA	Canada	IT	Italy	NE	Niger	UZ	Uzbekistan
CF	Central African Republic	JP	Japan	NL	Netherlands	VN	Viet Nam
CG	Congo	KE	Kenya	NO	Norway	YU	Yugoslavia
CH	Switzerland	KG	Kyrgyzstan	NZ	New Zealand	ZW	Zimbabwe
CI	Côte d'Ivoire	KP	Democratic People's Republic of Korea	PL	Poland		
CM	Cameroon	KR	Republis of Korea	PT	Portugal		
CN	China	KZ	Kazakstan	RO	Romania		
CU	Cuba	LC	Saint Lucia	RU	Russian Federation		
CZ	Czech Republic	LI	Liechtenstein	SD	Sudan		
DE	Germany	LK	Sri Lanka	SE	Sweden		
DK	Denmark	LR	Liberia	SG	Singapore		
EE	Estonia						

**COMPOUNDS FOR IMMUNOTHERAPY
OF PROSTATE CANCER AND METHODS FOR THEIR USE**

TECHNICAL FIELD

The present invention relates generally to compositions and methods for the treatment of prostate cancer. The invention is more particularly related to polypeptides comprising at least a portion of a prostate protein and to DNA molecules encoding such polypeptides. Such polypeptides may be used in vaccines and pharmaceutical compositions for treatment of prostate cancer.

BACKGROUND OF THE INVENTION

Prostate cancer is the most common form of cancer among males, with an estimated incidence of 30% in men over the age of 50. Overwhelming clinical evidence shows that human prostate cancer has the propensity to metastasize to bone, and the disease appears to progress inevitably from androgen dependent to androgen refractory status, leading to increased patient mortality. This prevalent disease is currently the second leading cause of cancer death among men in the U.S.

In spite of considerable research into therapies for the disease, prostate cancer remains difficult to treat. Commonly, treatment is based on surgery and/or radiation therapy, but these methods are ineffective in a significant percentage of cases. Two previously identified prostate specific proteins - prostate specific antigen (PSA) and prostatic acid phosphatase (PAP) - have limited therapeutic and diagnostic potential. For example, PSA levels do not always correlate well with the presence of prostate cancer, being positive in a percentage of non-prostate cancer cases, including benign prostatic hyperplasia (BPH). Furthermore, PSA measurements correlate with prostate volume, and do not indicate the level of metastasis.

Accordingly, there remains a need in the art for improved vaccines and treatment methods for prostate cancer.

SUMMARY OF THE INVENTION

The present invention provides compounds and methods for immunotherapy of prostate cancer. In one aspect, polypeptides are provided comprising at least an immunogenic portion of a prostate tumor protein or a variant of said protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants thereof.

In related aspects, DNA molecules encoding the above polypeptides are provided. In specific embodiments, such DNA molecules include sequences provided in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224. The present invention further provides expression vectors comprising the above DNA molecules and host cells transformed or transfected with such expression vectors. In preferred embodiments, the host cells are selected from the group consisting of *E. coli*, yeast and mammalian cells.

In another aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, an inventive polypeptide and a known prostate antigen.

The present invention also provides pharmaceutical compositions comprising one or more of the above polypeptides, or a DNA molecule encoding such polypeptides, and a physiologically acceptable carrier, together with vaccines comprising one or more of such polypeptide or DNA molecules in combination with a non-specific immune response enhancer.

In related aspects, pharmaceutical compositions for the treatment of prostate cancer comprising one or more polypeptides and a physiologically acceptable carrier are provided, wherein the polypeptide comprises an immunogenic portion of a prostate tumor protein or of a variant of said protein that differs only in conservative substitutions and/or modifications, the prostate tumor protein being encoded by a DNA molecule having a

sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants thereof. The invention also provides vaccines for the treatment of prostate cancer comprising such polypeptides in combination with a non-specific immune response enhancer, together with pharmaceutical compositions and vaccines comprising one or more DNA molecules having a sequence provided in SEQ ID NO: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106 and 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221. Pharmaceutical compositions and vaccines comprising one or more of the above fusion proteins are also provided.

In yet another aspect, methods are provided for inhibiting the development of prostate cancer in a patient, comprising administering an effective amount of at least one of the above pharmaceutical compositions and/or vaccines.

These and other aspects of the present invention will become apparent upon reference to the following detailed description and attached drawings. All references disclosed herein are hereby incorporated by reference in their entirety as if each was incorporated individually.

DETAILED DESCRIPTION OF THE INVENTION

As noted above, the present invention is generally directed to compositions and methods for the immunotherapy of prostate cancer. The inventive compositions are generally polypeptides that comprise at least a portion of a prostate tumor protein. Also included within the present invention are molecules (such as an antibody or fragment thereof) that bind to the inventive polypeptides. Such molecules are referred to herein as "binding agents."

In particular, the subject invention discloses polypeptides comprising at least a portion of a human prostate tumor protein, or a variant of such a protein that differs only in conservative substitutions and/or modifications, wherein the prostate tumor protein includes an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NO: 2, 3, 8-29, 41-45, 47-52, 54-

65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 181, 188, 191, 193, 194, 198, 203, 204, and 207-224, the complements of said nucleotide sequences and variants thereof. As used herein, the term "polypeptide" encompasses amino acid chains of any length, including full length proteins, wherein the amino acid residues are linked by covalent peptide bonds. Thus, a polypeptide comprising a portion of one of the above prostate proteins may consist entirely of the portion, or the portion may be present within a larger polypeptide that contains additional sequences. The additional sequences may be derived from the native protein or may be heterologous, and such sequences may be immunoreactive and/or antigenic.

As used herein, an "immunogenic portion" of a human prostate tumor protein is a portion that is capable of eliciting an immune response in a patient inflicted with prostate cancer and as such binds to antibodies present within sera from a prostate cancer patient. Immunogenic portions of the proteins described herein may thus be identified in antibody binding assays. Such assays may generally be performed using any of a variety of means known to those of ordinary skill in the art, as described, for example, in Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, Cold Spring Harbor, NY, 1988. For example, a polypeptide may be immobilized on a solid support (as described below) and contacted with patient sera to allow binding of antibodies within the sera to the immobilized polypeptide. Unbound sera may then be removed and bound antibodies detected using, for example, ¹²⁵I-labeled Protein A. Alternatively, a polypeptide may be used to generate monoclonal and polyclonal antibodies for use in detection of the polypeptide in blood or other fluids of prostate cancer patients.

The compositions and methods of the present invention also encompass variants of the above polypeptides and DNA molecules. A polypeptide "variant," as used herein, is a polypeptide that differs from the recited polypeptide only in conservative substitutions and/or modifications, such that the therapeutic, antigenic and/or immunogenic properties of the polypeptide are retained. Polypeptide variants preferably exhibit at least about 70%, more preferably at least about 90% and most preferably at least about 95% identity to the identified polypeptides. For prostate tumor polypeptides with immunoreactive properties, variants may, alternatively, be identified by modifying the amino acid sequence of

one of the above polypeptides, and evaluating the immunoreactivity of the modified polypeptide. For prostate tumor polypeptides useful for the generation of diagnostic binding agents, a variant may be identified by evaluating a modified polypeptide for the ability to generate antibodies that detect the presence or absence of prostate cancer. Such modified sequences may be prepared and tested using, for example, the representative procedures described herein.

As used herein, a "conservative substitution" is one in which an amino acid is substituted for another amino acid that has similar properties, such that one skilled in the art of peptide chemistry would expect the secondary structure and hydropathic nature of the polypeptide to be substantially unchanged. In general, the following groups of amino acids represent conservative changes: (1) ala, pro, gly, glu, asp, gln, asn, ser, thr; (2) cys, ser, tyr, thr; (3) val, ile, leu, met, ala, phe; (4) lys, arg, his; and (5) phe, tyr, trp, his.

Variants may also, or alternatively, contain other modifications, including the deletion or addition of amino acids that have minimal influence on the antigenic properties, secondary structure and hydropathic nature of the polypeptide. For example, a polypeptide may be conjugated to a signal (or leader) sequence at the N-terminal end of the protein which co-translationally or post-translationally directs transfer of the protein. The polypeptide may also be conjugated to a linker or other sequence for ease of synthesis, purification or identification of the polypeptide (e.g., poly-His), or to enhance binding of the polypeptide to a solid support. For example, a polypeptide may be conjugated to an immunoglobulin Fc region.

A nucleotide "variant" is a sequence that differs from the recited nucleotide sequence in having one or more nucleotide deletions, substitutions or additions. Such modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983). Nucleotide variants may be naturally occurring allelic variants, or non-naturally occurring variants. Variant nucleotide sequences preferably exhibit at least about 70%, more preferably at least about 80% and most preferably at least about 90% identity to the recited sequence. Such variant nucleotide sequences will generally hybridize to the recited nucleotide sequence under stringent conditions. As used herein, "stringent conditions" refers

to prewashing in a solution of 6X SSC, 0.2% SDS; hybridizing at 65 °C, 6X SSC, 0.2% SDS overnight; followed by two washes of 30 minutes each in 1X SSC, 0.1% SDS at 65 °C and two washes of 30 minutes each in 0.2X SSC, 0.1% SDS at 65 °C.

"Polypeptides" as used herein also include combination, or fusion, polypeptides. A "combination polypeptide" is a polypeptide comprising at least one of the above immunogenic portions and one or more additional immunogenic prostate tumor-specific sequences, which are joined via a peptide linkage into a single amino acid chain. The sequences may be joined directly (*i.e.*, with no intervening amino acids) or may be joined by way of a linked sequence (*e.g.*, Gly-Cys-Gly) that does not significantly diminish the immunogenic properties of the component polypeptides.

The prostate tumor proteins of the present invention, and DNA molecules encoding such proteins, may be isolated from prostate tumor tissue using any of a variety of methods well known in the art. DNA sequences corresponding to a gene (of a portion thereof) encoding one of the inventive prostate tumor proteins may be isolated from a prostate tumor cDNA library using a subtraction technique as described in detail below. Examples of such DNA sequences are provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Partial DNA sequences thus obtained may be used to design oligonucleotide primers for the amplification of full-length DNA sequences in a polymerase chain reaction (PCR), using techniques well known in the art (see, for example, Mullis et al., *Cold Spring Harbor Symp. Quant. Biol.*, 51:263, 1987; Erlich ed., *PCR Technology*, Stockton Press, NY, 1989). Once a DNA sequence encoding a polypeptide is obtained, any of the above modifications may be readily introduced using standard mutagenesis techniques, such as oligonucleotide-directed site-specific mutagenesis as taught, for example, by Adelman et al. (*DNA*, 2:183, 1983).

The prostate tumor polypeptides disclosed herein may also be generated by synthetic or recombinant means. Synthetic polypeptides having fewer than about 100 amino acids, and generally fewer than about 50 amino acids, may be generated using techniques well known to those of ordinary skill in the art. For example, such polypeptides may be synthesized using any of the commercially available solid-phase techniques, such as the Merrifield solid-phase synthesis method, where amino acids are sequentially added to a

growing amino acid chain (see, for example, Merrifield, *J. Am. Chem. Soc.* 85:2149-2146, 1963). Equipment for automated synthesis of polypeptides is commercially available from suppliers such as Perkin Elmer/Applied BioSystems Division (Foster City, CA), and may be operated according to the manufacturer's instructions.

Alternatively, any of the above polypeptides may be produced recombinantly by inserting a DNA sequence that encodes the polypeptide into an expression vector and expressing the protein in an appropriate host. Any of a variety of expression vectors known to those of ordinary skill in the art may be employed to express recombinant polypeptides of this invention. Expression may be achieved in any appropriate host cell that has been transformed or transfected with an expression vector containing a DNA molecule that encodes a recombinant polypeptide. Suitable host cells include prokaryotes, yeast and higher eukaryotic cells. Preferably, the host cells employed are *E. coli*, yeast or a mammalian cell line, such as CHO cells. The DNA sequences expressed in this manner may encode naturally occurring polypeptides, portions of naturally occurring polypeptides, or other variants thereof.

In general, regardless of the method of preparation, the polypeptides disclosed herein are prepared in substantially pure form (*i.e.*, the polypeptides are homogenous as determined by amino acid composition and primary sequence analysis). Preferably, the polypeptides are at least about 90% pure, more preferably at least about 95% pure and most preferably at least about 99% pure. In certain preferred embodiments, described in more detail below, the substantially pure polypeptides are incorporated into pharmaceutical compositions or vaccines for use in one or more of the methods disclosed herein.

In a related aspect, the present invention provides fusion proteins comprising a first and a second inventive polypeptide or, alternatively, a polypeptide of the present invention and a known prostate antigen, together with variants of such fusion proteins. The fusion proteins of the present invention may also include a linker peptide between the first and second polypeptides.

A DNA sequence encoding a fusion protein of the present invention is constructed using known recombinant DNA techniques to assemble separate DNA sequences encoding the first and second polypeptides into an appropriate expression vector. The 3' end

of a DNA sequence encoding the first polypeptide is ligated, with or without a peptide linker, to the 5' end of a DNA sequence encoding the second polypeptide so that the reading frames of the sequences are in phase to permit mRNA translation of the two DNA sequences into a single fusion protein that retains the biological activity of both the first and the second polypeptides.

A peptide linker sequence may be employed to separate the first and the second polypeptides by a distance sufficient to ensure that each polypeptide folds into its secondary and tertiary structures. Such a peptide linker sequence is incorporated into the fusion protein using standard techniques well known in the art. Suitable peptide linker sequences may be chosen based on the following factors: (1) their ability to adopt a flexible extended conformation; (2) their inability to adopt a secondary structure that could interact with functional epitopes on the first and second polypeptides; and (3) the lack of hydrophobic or charged residues that might react with the polypeptide functional epitopes. Preferred peptide linker sequences contain Gly, Asn and Ser residues. Other near neutral amino acids, such as Thr and Ala may also be used in the linker sequence. Amino acid sequences which may be usefully employed as linkers include those disclosed in Maratea et al., *Gene* 40:39-46, 1985; Murphy et al., *Proc. Natl. Acad. Sci. USA* 83:8258-8262, 1986; U.S. Patent No. 4,935,233 and U.S. Patent No. 4,751,180. The linker sequence may be from 1 to about 50 amino acids in length. Peptide sequences are not required when the first and second polypeptides have non-essential N-terminal amino acid regions that can be used to separate the functional domains and prevent steric interference.

The ligated DNA sequences are operably linked to suitable transcriptional or translational regulatory elements. The regulatory elements responsible for expression of DNA are located only 5' to the DNA sequence encoding the first polypeptides. Similarly, stop codons require to end translation and transcription termination signals are only present 3' to the DNA sequence encoding the second polypeptide.

Polypeptides of the present invention that comprise an immunogenic portion of a prostate tumor protein may generally be used for immunotherapy of prostate cancer, wherein the polypeptide stimulates the patient's own immune response to prostate tumor cells. In further aspects, the present invention provides methods for using one or more of the

immunoreactive polypeptides encoded by a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224 (or fusion proteins comprising one or more such polypeptides and/or DNA encoding such polypeptides) for immunotherapy of prostate cancer in a patient. As used herein, a "patient" refers to any warm-blooded animal, preferably a human. A patient may be afflicted with a disease, or may be free of detectable disease. Accordingly, the above immunoreactive polypeptides (or fusion proteins or DNA molecules encoding such polypeptides) may be used to treat prostate cancer or to inhibit the development of prostate cancer. The polypeptides may be administered either prior to or following surgical removal of primary tumors and/or treatment by administration of radiotherapy and conventional chemotherapeutic drugs.

In these aspects, the polypeptide or fusion protein is generally present within a pharmaceutical composition and/or a vaccine. Pharmaceutical compositions may comprise one or more polypeptides, each of which may contain one or more of the above sequences (or variants thereof), and a physiologically acceptable carrier. The vaccines may comprise one or more of such polypeptides and a non-specific immune response enhancer, such as an adjuvant, biodegradable microsphere (e.g., polylactic galactide) or a liposome (into which the polypeptide is incorporated). Pharmaceutical compositions and vaccines may also contain other epitopes of prostate tumor antigens, either incorporated into a combination polypeptide (*i.e.*, a single polypeptide that contains multiple epitopes) or present within a separate polypeptide.

Alternatively, a pharmaceutical composition or vaccine may contain DNA encoding one or more of the above polypeptides, such that the polypeptide is generated *in situ*. In such pharmaceutical compositions and vaccines, the DNA may be present within any of a variety of delivery systems known to those of ordinary skill in the art, including nucleic acid expression systems, bacteria and viral expression systems. Appropriate nucleic acid expression systems contain the necessary DNA sequences for expression in the patient (such as a suitable promoter). Bacterial delivery systems involve the administration of a bacterium (such as *Bacillus-Calmette-Guerrin*) that expresses an epitope of a prostate cell antigen on its cell surface. In a preferred embodiment, the DNA may be introduced using a viral expression system (e.g., vaccinia or other pox virus, retrovirus, or adenovirus), which may involve the

use of a non-pathogenic (defective), replication competent virus. Suitable systems are disclosed, for example, in Fisher-Hoch et al., *PNAS* 86:317-321, 1989; Flexner et al., *Ann. N.Y. Acad. Sci.* 569:86-103, 1989; Flexner et al., *Vaccine* 8:17-21, 1990; U.S. Patent Nos. 4,603,112, 4,769,330, and 5,017,487; WO 89/01973; U.S. Patent No. 4,777,127; GB 2,200,651; EP 0,345,242; WO 91/02805; Berkner, *Biotechniques* 6:616-627, 1988; Rosenfeld et al., *Science* 252:431-434, 1991; Kolls et al., *PNAS* 91:215-219, 1994; Kass-Eisler et al., *PNAS* 90:11498-11502, 1993; Guzman et al., *Circulation* 88:2838-2848, 1993; and Guzman et al., *Cir. Res.* 73:1202-1207, 1993. Techniques for incorporating DNA into such expression systems are well known to those of ordinary skill in the art. The DNA may also be "naked," as described, for example, in published PCT application WO 90/11092, and Ulmer et al., *Science* 259:1745-1749, 1993, reviewed by Cohen, *Science* 259:1691-1692, 1993. The uptake of naked DNA may be increased by coating the DNA onto biodegradable beads, which are efficiently transported into the cells.

Routes and frequency of administration, as well as dosage, will vary from individual to individual and may parallel those currently being used in immunotherapy of other diseases. In general, the pharmaceutical compositions and vaccines may be administered by injection (*e.g.*, intracutaneous, intramuscular, intravenous or subcutaneous), intranasally (*e.g.*, by aspiration) or orally. Between 1 and 10 doses may be administered over a 3-24 week period. Preferably, 4 doses are administered, at an interval of 3 months, and booster administrations may be given periodically thereafter. Alternate protocols may be appropriate for individual patients. A suitable dose is an amount of polypeptide or DNA that is effective to raise an immune response (cellular and/or humoral) against prostate tumor cells in a treated patient. A suitable immune response is at least 10-50% above the basal (*i.e.*, untreated) level. In general, the amount of polypeptide present in a dose (or produced *in situ* by the DNA in a dose) ranges from about 1 pg to about 100 mg per kg of host, typically from about 10 pg to about 1 mg, and preferably from about 100 pg to about 1 μ g. Suitable dose sizes will vary with the size of the patient, but will typically range from about 0.01 mL to about 5 mL.

While any suitable carrier known to those of ordinary skill in the art may be employed in the pharmaceutical compositions of this invention, the type of carrier will vary

depending on the mode of administration. For parenteral administration, such as subcutaneous injection, the carrier preferably comprises water, saline, alcohol, a lipid, a wax and/or a buffer. For oral administration, any of the above carriers or a solid carrier, such as mannitol, lactose, starch, magnesium stearate, sodium saccharine, talcum, cellulose, glucose, sucrose, and/or magnesium carbonate, may be employed. Biodegradable microspheres (e.g., polylactic glycolide) may also be employed as carriers for the pharmaceutical compositions of this invention. Suitable biodegradable microspheres are disclosed, for example, in U.S. Patent Nos. 4,897,268 and 5,075,109.

Any of a variety of non-specific immune response enhancers may be employed in the vaccines of this invention. For example, an adjuvant may be included. Most adjuvants contain a substance designed to protect the antigen from rapid catabolism, such as aluminum hydroxide or mineral oil, and a nonspecific stimulator of immune response, such as lipid A, *Bordetella pertussis* or *Mycobacterium tuberculosis*. Such adjuvants are commercially available as, for example, Freund's Incomplete Adjuvant and Complete Adjuvant (Difco Laboratories, Detroit, MI) and Merck Adjuvant 65 (Merck and Company, Inc., Rahway, NJ).

Polypeptides disclosed herein may also be employed in *ex vivo* treatment of prostate cancer. For example, cells of the immune system, such as T cells, may be isolated from the peripheral blood of a patient, using a commercially available cell separation system, such as CellPro Incorporated's (Bothell, WA) CEPRATETM system (see U.S. Patent No. 5,240,856; U.S. Patent No. 5,215,926; WO 89/06280; WO 91/16116 and WO 92/07243). The separated cells are stimulated with one or more of the immunoreactive polypeptides contained within a delivery vehicle, such as a microsphere, to provide antigen-specific T cells. The population of tumor antigen-specific T cells is then expanded using standard techniques and the cells are administered back to the patient.

Polypeptides of the present invention may also, or alternatively, be used to generate binding agents, such as antibodies or fragments thereof, that are capable of detecting metastatic human prostate tumors. Binding agents of the present invention may generally be prepared using methods known to those of ordinary skill in the art, including the representative procedures described herein. Binding agents are capable of differentiating between patients with and without prostate cancer, using the representative assays described

herein. In other words, antibodies or other binding agents raised against a prostate tumor protein, or a suitable portion thereof, will generate a signal indicating the presence of primary or metastatic prostate cancer in at least about 20% of patients afflicted with the disease, and will generate a negative signal indicating the absence of the disease in at least about 90% of individuals without primary or metastatic prostate cancer. Suitable portions of such prostate tumor proteins are portions that are able to generate a binding agent that indicates the presence of primary or metastatic prostate cancer in substantially all (*i.e.*, at least about 80%, and preferably at least about 90%) of the patients for which prostate cancer would be indicated using the full length protein, and that indicate the absence of prostate cancer in substantially all of those samples that would be negative when tested with full length protein. The representative assays described below, such as the two-antibody sandwich assay, may generally be employed for evaluating the ability of a binding agent to detect metastatic human prostate tumors.

The ability of a polypeptide prepared as described herein to generate antibodies capable of detecting primary or metastatic human prostate tumors may generally be evaluated by raising one or more antibodies against the polypeptide (using, for example, a representative method described herein) and determining the ability of such antibodies to detect such tumors in patients. This determination may be made by assaying biological samples from patients with and without primary or metastatic prostate cancer for the presence of a polypeptide that binds to the generated antibodies. Such test assays may be performed, for example, using a representative procedure described below. Polypeptides that generate antibodies capable of detecting at least 20% of primary or metastatic prostate tumors by such procedures are considered to be useful in assays for detecting primary or metastatic human prostate tumors. Polypeptide specific antibodies may be used alone or in combination to improve sensitivity.

Polypeptides capable of detecting primary or metastatic human prostate tumors may be used as markers for diagnosing prostate cancer or for monitoring disease progression in patients. In one embodiment, prostate cancer in a patient may be diagnosed by evaluating a biological sample obtained from the patient for the level of one or more of the

above polypeptides, relative to a predetermined cut-off value. As used herein, suitable "biological samples" include blood, sera, urine and/or prostate secretions.

The level of one or more of the above polypeptides may be evaluated using any binding agent specific for the polypeptide(s). A "binding agent," in the context of this invention, is any agent (such as a compound or a cell) that binds to a polypeptide as described above. As used herein, "binding" refers to a noncovalent association between two separate molecules (each of which may be free (*i.e.*, in solution) or present on the surface of a cell or a solid support), such that a "complex" is formed. Such a complex may be free or immobilized (either covalently or noncovalently) on a support material. The ability to bind may generally be evaluated by determining a binding constant for the formation of the complex. The binding constant is the value obtained when the concentration of the complex is divided by the product of the component concentrations. In general, two compounds are said to "bind" in the context of the present invention when the binding constant for complex formation exceeds about 10^3 L/mol. The binding constant may be determined using methods well known to those of ordinary skill in the art.

Any agent that satisfies the above requirements may be a binding agent. For example, a binding agent may be a ribosome with or without a peptide component, an RNA molecule or a peptide. In a preferred embodiment, the binding partner is an antibody, or a fragment thereof. Such antibodies may be polyclonal, or monoclonal. In addition, the antibodies may be single chain, chimeric, CDR-grafted or humanized. Antibodies may be prepared by the methods described herein and by other methods well known to those of skill in the art.

There are a variety of assay formats known to those of ordinary skill in the art for using a binding partner to detect polypeptide markers in a sample. *See, e.g.*, Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In a preferred embodiment, the assay involves the use of binding partner immobilized on a solid support to bind to and remove the polypeptide from the remainder of the sample. The bound polypeptide may then be detected using a second binding partner that contains a reporter group. Suitable second binding partners include antibodies that bind to the binding partner/polypeptide complex. Alternatively, a competitive assay may be utilized, in which a

polypeptide is labeled with a reporter group and allowed to bind to the immobilized binding partner after incubation of the binding partner with the sample. The extent to which components of the sample inhibit the binding of the labeled polypeptide to the binding partner is indicative of the reactivity of the sample with the immobilized binding partner.

The solid support may be any material known to those of ordinary skill in the art to which the antigen may be attached. For example, the solid support may be a test well in a microtiter plate or a nitrocellulose or other suitable membrane. Alternatively, the support may be a bead or disc, such as glass, fiberglass, latex or a plastic material such as polystyrene or polyvinylchloride. The support may also be a magnetic particle or a fiber optic sensor, such as those disclosed, for example, in U.S. Patent No. 5,359,681. The binding agent may be immobilized on the solid support using a variety of techniques known to those of skill in the art, which are amply described in the patent and scientific literature. In the context of the present invention, the term "immobilization" refers to both noncovalent association, such as adsorption, and covalent attachment (which may be a direct linkage between the antigen and functional groups on the support or may be a linkage by way of a cross-linking agent). Immobilization by adsorption to a well in a microtiter plate or to a membrane is preferred. In such cases, adsorption may be achieved by contacting the binding agent, in a suitable buffer, with the solid support for a suitable amount of time. The contact time varies with temperature, but is typically between about 1 hour and about 1 day. In general, contacting a well of a plastic microtiter plate (such as polystyrene or polyvinylchloride) with an amount of binding agent ranging from about 10 ng to about 10 µg, and preferably about 100 ng to about 1 µg, is sufficient to immobilize an adequate amount of binding agent.

Covalent attachment of binding agent to a solid support may generally be achieved by first reacting the support with a bifunctional reagent that will react with both the support and a functional group, such as a hydroxyl or amino group, on the binding agent. For example, the binding agent may be covalently attached to supports having an appropriate polymer coating using benzoquinone or by condensation of an aldehyde group on the support with an amine and an active hydrogen on the binding partner (*see, e.g.,* Pierce Immunotechnology Catalog and Handbook, 1991, at A12-A13).

In certain embodiments, the assay is a two-antibody sandwich assay. This assay may be performed by first contacting an antibody that has been immobilized on a solid support, commonly the well of a microtiter plate, with the sample, such that polypeptides within the sample are allowed to bind to the immobilized antibody. Unbound sample is then removed from the immobilized polypeptide-antibody complexes and a second antibody (containing a reporter group) capable of binding to a different site on the polypeptide is added. The amount of second antibody that remains bound to the solid support is then determined using a method appropriate for the specific reporter group.

More specifically, once the antibody is immobilized on the support as described above, the remaining protein binding sites on the support are typically blocked. Any suitable blocking agent known to those of ordinary skill in the art, such as bovine serum albumin or Tween 20TM (Sigma Chemical Co., St. Louis, MO). The immobilized antibody is then incubated with the sample, and polypeptide is allowed to bind to the antibody. The sample may be diluted with a suitable diluent, such as phosphate-buffered saline (PBS) prior to incubation. In general, an appropriate contact time (*i.e.*, incubation time) is that period of time that is sufficient to detect the presence of polypeptide within a sample obtained from an individual with prostate cancer. Preferably, the contact time is sufficient to achieve a level of binding that is at least about 95% of that achieved at equilibrium between bound and unbound polypeptide. Those of ordinary skill in the art will recognize that the time necessary to achieve equilibrium may be readily determined by assaying the level of binding that occurs over a period of time. At room temperature, an incubation time of about 30 minutes is generally sufficient.

Unbound sample may then be removed by washing the solid support with an appropriate buffer, such as PBS containing 0.1% Tween 20TM. The second antibody, which contains a reporter group, may then be added to the solid support. Preferred reporter groups include enzymes (such as horseradish peroxidase), substrates, cofactors, inhibitors, dyes, radionuclides, luminescent groups, fluorescent groups and biotin. The conjugation of antibody to reporter group may be achieved using standard methods known to those of ordinary skill in the art.

The second antibody is then incubated with the immobilized antibody-polypeptide complex for an amount of time sufficient to detect the bound polypeptide. An appropriate amount of time may generally be determined by assaying the level of binding that occurs over a period of time. Unbound second antibody is then removed and bound second antibody is detected using the reporter group. The method employed for detecting the reporter group depends upon the nature of the reporter group. For radioactive groups, scintillation counting or autoradiographic methods are generally appropriate. Spectroscopic methods may be used to detect dyes, luminescent groups and fluorescent groups. Biotin may be detected using avidin, coupled to a different reporter group (commonly a radioactive or fluorescent group or an enzyme). Enzyme reporter groups may generally be detected by the addition of substrate (generally for a specific period of time), followed by spectroscopic or other analysis of the reaction products.

To determine the presence or absence of prostate cancer, the signal detected from the reporter group that remains bound to the solid support is generally compared to a signal that corresponds to a predetermined cut-off value. In one preferred embodiment, the cut-off value is the average mean signal obtained when the immobilized antibody is incubated with samples from patients without prostate cancer. In general, a sample generating a signal that is three standard deviations above the predetermined cut-off value is considered positive for prostate cancer. In an alternate preferred embodiment, the cut-off value is determined using a Receiver Operator Curve, according to the method of Sackett et al., *Clinical Epidemiology: A Basic Science for Clinical Medicine*, Little Brown and Co., 1985, p. 106-7. Briefly, in this embodiment, the cut-off value may be determined from a plot of pairs of true positive rates (*i.e.*, sensitivity) and false positive rates (100%-specificity) that correspond to each possible cut-off value for the diagnostic test result. The cut-off value on the plot that is the closest to the upper left-hand corner (*i.e.*, the value that encloses the largest area) is the most accurate cut-off value, and a sample generating a signal that is higher than the cut-off value determined by this method may be considered positive. Alternatively, the cut-off value may be shifted to the left along the plot, to minimize the false positive rate, or to the right, to minimize the false negative rate. In general, a sample generating a signal that is higher than the cut-off value determined by this method is considered positive for prostate cancer.

In a related embodiment, the assay is performed in a flow-through or strip test format, wherein the antibody is immobilized on a membrane, such as nitrocellulose. In the flow-through test, polypeptides within the sample bind to the immobilized antibody as the sample passes through the membrane. A second, labeled antibody then binds to the antibody-polypeptide complex as a solution containing the second antibody flows through the membrane. The detection of bound second antibody may then be performed as described above. In the strip test format, one end of the membrane to which antibody is bound is immersed in a solution containing the sample. The sample migrates along the membrane through a region containing second antibody and to the area of immobilized antibody. Concentration of second antibody at the area of immobilized antibody indicates the presence of prostate cancer. Typically, the concentration of second antibody at that site generates a pattern, such as a line, that can be read visually. The absence of such a pattern indicates a negative result. In general, the amount of antibody immobilized on the membrane is selected to generate a visually discernible pattern when the biological sample contains a level of polypeptide that would be sufficient to generate a positive signal in the two-antibody sandwich assay, in the format discussed above. Preferably, the amount of antibody immobilized on the membrane ranges from about 25 ng to about 1 µg, and more preferably from about 50 ng to about 500 ng. Such tests can typically be performed with a very small amount of biological sample.

Of course, numerous other assay protocols exist that are suitable for use with the antigens or antibodies of the present invention. The above descriptions are intended to be exemplary only.

In another embodiment, the above polypeptides may be used as markers for the progression of prostate cancer. In this embodiment, assays as described above for the diagnosis of prostate cancer may be performed over time, and the change in the level of reactive polypeptide(s) evaluated. For example, the assays may be performed every 24-72 hours for a period of 6 months to 1 year, and thereafter performed as needed. In general, prostate cancer is progressing in those patients in whom the level of polypeptide detected by the binding agent increases over time. In contrast, prostate cancer is not progressing when the level of reactive polypeptide either remains constant or decreases with time.

Antibodies for use in the above methods may be prepared by any of a variety of techniques known to those of ordinary skill in the art. See, e.g., Harlow and Lane, *Antibodies: A Laboratory Manual*, Cold Spring Harbor Laboratory, 1988. In one such technique, an immunogen comprising the antigenic polypeptide is initially injected into any of a wide variety of mammals (e.g., mice, rats, rabbits, sheep and goats). In this step, the polypeptides of this invention may serve as the immunogen without modification. Alternatively, particularly for relatively short polypeptides, a superior immune response may be elicited if the polypeptide is joined to a carrier protein, such as bovine serum albumin or keyhole limpet hemocyanin. The immunogen is injected into the animal host, preferably according to a predetermined schedule incorporating one or more booster immunizations, and the animals are bled periodically. Polyclonal antibodies specific for the polypeptide may then be purified from such antisera by, for example, affinity chromatography using the polypeptide coupled to a suitable solid support.

Monoclonal antibodies specific for the antigenic polypeptide of interest may be prepared, for example, using the technique of Kohler and Milstein, *Eur. J. Immunol.* 6:511-519, 1976, and improvements thereto. Briefly, these methods involve the preparation of immortal cell lines capable of producing antibodies having the desired specificity (*i.e.*, reactivity with the polypeptide of interest). Such cell lines may be produced, for example, from spleen cells obtained from an animal immunized as described above. The spleen cells are then immortalized by, for example, fusion with a myeloma cell fusion partner, preferably one that is syngeneic with the immunized animal. A variety of fusion techniques may be employed. For example, the spleen cells and myeloma cells may be combined with a nonionic detergent for a few minutes and then plated at low density on a selective medium that supports the growth of hybrid cells, but not myeloma cells. A preferred selection technique uses HAT (hypoxanthine, aminopterin, thymidine) selection. After a sufficient time, usually about 1 to 2 weeks, colonies of hybrids are observed. Single colonies are selected and tested for binding activity against the polypeptide. Hybridomas having high reactivity and specificity are preferred.

Monoclonal antibodies may be isolated from the supernatants of growing hybridoma colonies. In addition, various techniques may be employed to enhance the yield,

such as injection of the hybridoma cell line into the peritoneal cavity of a suitable vertebrate host, such as a mouse. Monoclonal antibodies may then be harvested from the ascites fluid or the blood. Contaminants may be removed from the antibodies by conventional techniques, such as chromatography, gel filtration, precipitation, and extraction. The polypeptides of this invention may be used in the purification process in, for example, an affinity chromatography step.

Monoclonal antibodies of the present invention may also be used as therapeutic reagents, to diminish or eliminate prostate tumors. The antibodies may be used on their own (for instance, to inhibit metastases) or coupled to one or more therapeutic agents. Suitable agents in this regard include radionuclides, differentiation inducers, drugs, toxins, and derivatives thereof. Preferred radionuclides include ^{90}Y , ^{123}I , ^{125}I , ^{131}I , ^{186}Re , ^{188}Re , ^{211}At , and ^{212}Bi . Preferred drugs include methotrexate, and pyrimidine and purine analogs. Preferred differentiation inducers include phorbol esters and butyric acid. Preferred toxins include ricin, abrin, diphtheria toxin, cholera toxin, gelonin, *Pseudomonas* exotoxin, *Shigella* toxin, and pokeweed antiviral protein.

A therapeutic agent may be coupled (*e.g.*, covalently bonded) to a suitable monoclonal antibody either directly or indirectly (*e.g.*, via a linker group). A direct reaction between an agent and an antibody is possible when each possesses a substituent capable of reacting with the other. For example, a nucleophilic group, such as an amino or sulphydryl group, on one may be capable of reacting with a carbonyl-containing group, such as an anhydride or an acid halide, or with an alkyl group containing a good leaving group (*e.g.*, a halide) on the other.

Alternatively, it may be desirable to couple a therapeutic agent and an antibody via a linker group. A linker group can function as a spacer to distance an antibody from an agent in order to avoid interference with binding capabilities. A linker group can also serve to increase the chemical reactivity of a substituent on an agent or an antibody, and thus increase the coupling efficiency. An increase in chemical reactivity may also facilitate the use of agents, or functional groups on agents, which otherwise would not be possible.

It will be evident to those skilled in the art that a variety of bifunctional or polyfunctional reagents, both homo- and hetero-functional (such as those described in the

catalog of the Pierce Chemical Co., Rockford, IL), may be employed as the linker group. Coupling may be effected, for example, through amino groups, carboxyl groups, sulfhydryl groups or oxidized carbohydrate residues. There are numerous references describing such methodology, *e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.

Where a therapeutic agent is more potent when free from the antibody portion of the immunoconjugates of the present invention, it may be desirable to use a linker group which is cleavable during or upon internalization into a cell. A number of different cleavable linker groups have been described. The mechanisms for the intracellular release of an agent from these linker groups include cleavage by reduction of a disulfide bond (*e.g.*, U.S. Patent No. 4,489,710, to Spitzer), by irradiation of a photolabile bond (*e.g.*, U.S. Patent No. 4,625,014, to Senter et al.), by hydrolysis of derivatized amino acid side chains (*e.g.*, U.S. Patent No. 4,638,045, to Kohn et al.), by serum complement-mediated hydrolysis (*e.g.*, U.S. Patent No. 4,671,958, to Rodwell et al.), and acid-catalyzed hydrolysis (*e.g.*, U.S. Patent No. 4,569,789, to Blattler et al.).

It may be desirable to couple more than one agent to an antibody. In one embodiment, multiple molecules of an agent are coupled to one antibody molecule. In another embodiment, more than one type of agent may be coupled to one antibody. Regardless of the particular embodiment, immunoconjugates with more than one agent may be prepared in a variety of ways. For example, more than one agent may be coupled directly to an antibody molecule, or linkers which provide multiple sites for attachment can be used. Alternatively, a carrier can be used.

A carrier may bear the agents in a variety of ways, including covalent bonding either directly or via a linker group. Suitable carriers include proteins such as albumins (*e.g.*, U.S. Patent No. 4,507,234, to Kato et al.), peptides and polysaccharides such as aminodextran (*e.g.*, U.S. Patent No. 4,699,784, to Shih et al.). A carrier may also bear an agent by noncovalent bonding or by encapsulation, such as within a liposome vesicle (*e.g.*, U.S. Patent Nos. 4,429,008 and 4,873,088). Carriers specific for radionuclide agents include radiohalogenated small molecules and chelating compounds. For example, U.S. Patent No. 4,735,792 discloses representative radiohalogenated small molecules and their synthesis. A radionuclide chelate may be formed from chelating compounds that include those containing

nitrogen and sulfur atoms as the donor atoms for binding the metal, or metal oxide, radionuclide. For example, U.S. Patent No. 4,673,562, to Davison et al. discloses representative chelating compounds and their synthesis.

A variety of routes of administration for the antibodies and immunoconjugates may be used. Typically, administration will be intravenous, intramuscular, subcutaneous or in the bed of a resected tumor. It will be evident that the precise dose of the antibody/immunoconjugate will vary depending upon the antibody used, the antigen density on the tumor, and the rate of clearance of the antibody.

Diagnostic reagents of the present invention may also comprise DNA sequences encoding one or more of the above polypeptides, or one or more portions thereof. For example, at least two oligonucleotide primers may be employed in a polymerase chain reaction (PCR) based assay to amplify prostate tumor-specific cDNA derived from a biological sample, wherein at least one of the oligonucleotide primers is specific for a DNA molecule encoding a prostate tumor protein of the present invention. The presence of the amplified cDNA is then detected using techniques well known in the art, such as gel electrophoresis. Similarly, oligonucleotide probes specific for a DNA molecule encoding a prostate tumor protein of the present invention may be used in a hybridization assay to detect the presence of an inventive polypeptide in a biological sample.

As used herein, the term "oligonucleotide primer/probe specific for a DNA molecule" means an oligonucleotide sequence that has at least about 80%, preferably at least about 90% and more preferably at least about 95%, identity to the DNA molecule in question. Oligonucleotide primers and/or probes which may be usefully employed in the inventive diagnostic methods preferably have at least about 10-40 nucleotides. In a preferred embodiment, the oligonucleotide primers comprise at least about 10 contiguous nucleotides of a DNA molecule having a sequence selected from SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Preferably, oligonucleotide probes for use in the inventive diagnostic methods comprise at least about 15 contiguous oligonucleotides of a DNA molecule having a sequence provided in SEQ ID NOS: 1-107, 109-111, 115-171, 173-175, 177 and 179-224. Techniques for both PCR based assays and hybridization assays are well known in the art (see, for example, Mullis *et al. Ibid*; Ehrlich, *Ibid*). Primers or probes may

thus be used to detect prostate tumor-specific sequences in biological samples, including blood, semen, prostate tissue and/or prostate tumor tissue.

The following Examples are offered by way of illustration and not by way of limitation.

EXAMPLES

Example 1

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES

This Example describes the isolation of prostate tumor polypeptides from a prostate tumor cDNA library.

A human prostate tumor cDNA expression library was constructed from prostate tumor poly A⁺ RNA using a Superscript Plasmid System for cDNA Synthesis and Plasmid Cloning kit (BRL Life Technologies, Gaithersburg, MD 20897) following the manufacturer's protocol. Specifically, prostate tumor tissues were homogenized with polytron (Kinematica, Switzerland) and total RNA was extracted using Trizol reagent (BRL Life Technologies) as directed by the manufacturer. The poly A⁺ RNA was then purified using a Qiagen oligotex spin column mRNA purification kit (Qiagen, Santa Clarita, CA 91355) according to the manufacturer's protocol. First-strand cDNA was synthesized using the NotI/Oligo-dT18 primer. Double-stranded cDNA was synthesized, ligated with EcoRI/BAXI adaptors (Invitrogen, San Diego, CA) and digested with NotI. Following size fractionation with Chroma Spin-1000 columns (Clontech, Palo Alto, CA 94303), the cDNA was ligated into the EcoRI/NotI site of pCDNA3.1 (Invitrogen) and transformed into ElectroMax *E. coli* DH10B cells (BRL Life Technologies) by electroporation.

Using the same procedure, a normal human pancreas cDNA expression library was prepared from a pool of six tissue specimens (Clontech). The cDNA libraries were characterized by determining the number of independent colonies, the percentage of clones that carried insert, the average insert size and by sequence analysis. The prostate tumor

library contained 1.64×10^7 independent colonies, with 70% of clones having an insert and the average insert size being 1745 base pairs. The normal pancreas cDNA library contained 3.3×10^6 independent colonies, with 69% of clones having inserts and the average insert size being 1120 base pairs. For both libraries, sequence analysis showed that the majority of clones had a full length cDNA sequence and were synthesized from mRNA, with minimal rRNA and mitochondrial DNA contamination.

cDNA library subtraction was performed using the above prostate tumor and normal pancreas cDNA libraries, as described by Hara *et al.* (*Blood*, 84:189-199, 1994) with some modifications. Specifically, a prostate tumor-specific subtracted cDNA library was generated as follows. Normal pancreas cDNA library (70 µg) was digested with EcoRI, NotI, and Sful, followed by a filling-in reaction with DNA polymerase Klenow fragment. After phenol-chloroform extraction and ethanol precipitation, the DNA was dissolved in 100 µl of H₂O, heat-denatured and mixed with 100 µl (100 µg) of Photoprobe biotin (Vector Laboratories, Burlingame, CA). As recommended by the manufacturer, the resulting mixture was irradiated with a 270 W sunlamp on ice for 20 minutes. Additional Photoprobe biotin (50 µl) was added and the biotinylation reaction was repeated. After extraction with butanol five times, the DNA was ethanol-precipitated and dissolved in 23 µl H₂O to form the driver DNA.

To form the tracer DNA, 10 µg prostate tumor cDNA library was digested with BamHI and XhoI, phenol chloroform extracted and passed through Chroma spin-400 columns (Clontech). Following ethanol precipitation, the tracer DNA was dissolved in 5 µl H₂O. Tracer DNA was mixed with 15 µl driver DNA and 20 µl of 2 x hybridization buffer (1.5 M NaCl/10 mM EDTA/50 mM HEPES pH 7.5/0.2% sodium dodecyl sulfate), overlaid with mineral oil, and heat-denatured completely. The sample was immediately transferred into a 68 °C water bath and incubated for 20 hours (long hybridization [LH]). The reaction mixture was then subjected to a streptavidin treatment followed by phenol/chloroform extraction. This process was repeated three more times. Subtracted DNA was precipitated, dissolved in 12 µl H₂O, mixed with 8 µl driver DNA and 20 µl of 2 x hybridization buffer, and subjected to a hybridization at 68 °C for 2 hours (short hybridization [SH]). After removal of biotinylated double-stranded DNA, subtracted cDNA was ligated into

BamHI/XhoI site of chloramphenicol resistant pBCSK⁺ (Stratagene, La Jolla, CA 92037) and transformed into ElectroMax *E. coli* DH10B cells by electroporation to generate a prostate tumor specific subtracted cDNA library (prostate subtraction 1).

To analyze the subtracted cDNA library, plasmid DNA was prepared from 100 independent clones, randomly picked from the subtracted prostate tumor specific library and grouped based on insert size. Representative cDNA clones were further characterized by DNA sequencing with a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A (Foster City, CA). Six cDNA clones, hereinafter referred to as F1-13, F1-12, F1-16, H1-1, H1-9 and H1-4, were shown to be abundant in the subtracted prostate-specific cDNA library. The determined 3' and 5' cDNA sequences for F1-12 are provided in SEQ ID NO: 2 and 3, respectively, with determined 3' cDNA sequences for F1-13, F1-16, H1-1, H1-9 and H1-4 being provided in SEQ ID NO: 1 and 4-7, respectively.

The cDNA sequences for the isolated clones were compared to known sequences in the gene bank using the EMBL and GenBank databases (release 96). Four of the prostate tumor cDNA clones, F1-13, F1-16, H1-1, and H1-4, were determined to encode the following previously identified proteins: prostate specific antigen (PSA), human glandular kallikrein, human tumor expression enhanced gene, and mitochondria cytochrome C oxidase subunit II. H1-9 was found to be identical to a previously identified human autonomously replicating sequence. No significant homologies to the cDNA sequence for F1-12 were found.

Subsequent studies led to the isolation of a full-length cDNA sequence for F1-12. This sequence is provided in SEQ ID NO: 107, with the corresponding predicted amino acid sequence being provided in SEQ ID NO: 108.

To clone less abundant prostate tumor specific genes, cDNA library subtraction was performed by subtracting the prostate tumor cDNA library described above with the normal pancreas cDNA library and with the three most abundant genes in the previously subtracted prostate tumor specific cDNA library: human glandular kallikrein, prostate specific antigen (PSA), and mitochondria cytochrome C oxidase subunit II. Specifically, 1 µg each of human glandular kallikrein, PSA and mitochondria cytochrome C oxidase subunit II cDNAs in pCDNA3.1 were added to the driver DNA and subtraction was

performed as described above to provide a second subtracted cDNA library hereinafter referred to as the "subtracted prostate tumor specific cDNA library with spike".

Twenty-two cDNA clones were isolated from the subtracted prostate tumor specific cDNA library with spike. The determined 3' and 5' cDNA sequences for the clones referred to as J1-17, L1-12, N1-1862, J1-13, J1-19, J1-25, J1-24, K1-58, K1-63, L1-4 and L1-14 are provided in SEQ ID NOS: 8-9, 10-11, 12-13, 14-15, 16-17, 18-19, 20-21, 22-23, 24-25, 26-27 and 28-29, respectively. The determined 3' cDNA sequences for the clones referred to as J1-12, J1-16, J1-21, K1-48, K1-55, L1-2, L1-6, N1-1858, N1-1860, N1-1861, N1-1864 are provided in SEQ ID NOS: 30-40, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to three of the five most abundant DNA species, (J1-17, L1-12 and N1-1862; SEQ ID NOS: 8-9, 10-11 and 12-13, respectively). Of the remaining two most abundant species, one (J1-12; SEQ ID NO:30) was found to be identical to the previously identified human pulmonary surfactant-associated protein, and the other (K1-48; SEQ ID NO:33) was determined to have some homology to *R. norvegicus* mRNA for 2-arylpropionyl-CoA epimerase. Of the 17 less abundant cDNA clones isolated from the subtracted prostate tumor specific cDNA library with spike, four (J1-16, K1-55, L1-6 and N1-1864; SEQ ID NOS:31, 34, 36 and 40, respectively) were found to be identical to previously identified sequences, two (J1-21 and N1-1860; SEQ ID NOS: 32 and 38, respectively) were found to show some homology to non-human sequences, and two (L1-2 and N1-1861; SEQ ID NOS: 35 and 39, respectively) were found to show some homology to known human sequences. No significant homologies were found to the polypeptides J1-13, J1-19, J1-24, J1-25, K1-58, K1-63, L1-4, L1-14 (SEQ ID NOS: 14-15, 16-17, 20-21, 18-19, 22-23, 24-25, 26-27, 28-29, respectively).

Subsequent studies led to the isolation of full length cDNA sequences for J1-17, L1-12 and N1-1862 (SEQ ID NOS: 109-111, respectively). The corresponding predicted amino acid sequences are provided in SEQ ID NOS: 112-114.

In a further experiment, four additional clones were identified by subtracting a prostate tumor cDNA library with normal prostate cDNA prepared from a pool of three normal prostate poly A+ RNA (prostate subtraction 2). The determined cDNA sequences for these clones; hereinafter referred to as U1-3064, U1-3065, V1-3692 and 1A-3905, are

provided in SEQ ID NO: 69-72, respectively. Comparison of the determined sequences with those in the gene bank revealed no significant homologies to U1-3065.

A second subtraction with spike (prostate subtraction spike 2) was performed by subtracting a prostate tumor specific cDNA library with spike with normal pancreas cDNA library and further spiked with PSA, J1-17, pulmonary surfactant-associated protein, mitochondrial DNA, cytochrome c oxidase subunit II, N1-1862, autonomously replicating sequence, L1-12 and tumor expression enhanced gene. Four additional clones, hereinafter referred to as V1-3686, R1-2330, 1B-3976 and V1-3679, were isolated. The determined cDNA sequences for these clones are provided in SEQ ID NO:73-76, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to V1-3686 and R1-2330.

Further analysis of the three prostate subtractions described above (prostate subtraction 2, subtracted prostate tumor specific cDNA library with spike, and prostate subtraction spike 2) resulted in the identification of sixteen additional clones, referred to as 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1G-4734, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4810, 1I-4811, 1J-4876, 1K-4884 and 1K-4896. The determined cDNA sequences for these clones are provided in SEQ ID NOS: 77-92, respectively. Comparison of these sequences with those in the gene bank as described above, revealed no significant homologies to 1G-4741, 1G-4734, 1I-4807, 1J-4876 and 1K-4896 (SEQ ID NOS: 79, 81, 87, 90 and 92, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4736, 1G-4738, 1G-4741, 1G-4744, 1H-4774, 1H-4781, 1H-4785, 1H-4787, 1H-4796, 1I-4807, 1J-4876, 1K-4884 and 1K-4896, provided in SEQ ID NOS: 179-188 and 191-193, respectively, and to the determination of additional partial cDNA sequences for 1I-4810 and 1I-4811, provided in SEQ ID NOS: 189 and 190, respectively.

An additional subtraction was performed by subtracting a normal prostate cDNA library with normal pancreas cDNA (prostate subtraction 3). This led to the identification of six additional clones referred to as 1G-4761, 1G-4762, 1H-4766, 1H-4770, 1H-4771 and 1H-4772 (SEQ ID NOS: 93-98). Comparison of these sequences with those in the gene bank revealed no significant homologies to 1G-4761 and 1H-4771 (SEQ ID NOS:

93 and 97, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1G-4761, 1G-4762, 1H-4766 and 1H-4772 provided in SEQ ID NOS: 194-196 and 199, respectively, and to the determination of additional partial cDNA sequences for 1H-4770 and 1H-4771, provided in SEQ ID NOS: 197 and 198, respectively.

Subtraction of a prostate tumor cDNA library, prepared from a pool of polyA+ RNA from three prostate cancer patients, with a normal pancreas cDNA library (prostate subtraction 4) led to the identification of eight clones, referred to as 1D-4297, 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280 (SEQ ID NOS: 99-107). These sequences were compared to those in the gene bank as described above. No significant homologies were found to 1D-4283 and 1D-4304 (SEQ ID NOS: 103 and 104, respectively). Further analysis of the isolated clones led to the determination of extended cDNA sequences for 1D-4309, 1D.1-4278, 1D-4288, 1D-4283, 1D-4304, 1D-4296 and 1D-4280, provided in SEQ ID NOS: 200-206, respectively. cDNA clones isolated in prostate subtraction 1 and prostate subtraction 2, described above, were colony PCR amplified and their mRNA expression levels in prostate tumor, normal prostate and in various other normal tissues were determined using microarray technology (Synteni, Palo Alto, CA). Briefly, the PCR amplification products were dotted onto slides in an array format, with each product occupying a unique location in the array. mRNA was extracted from the tissue sample to be tested, reverse transcribed, and fluorescent-labeled cDNA probes were generated. The microarrays were probed with the labeled cDNA probes, the slides scanned and fluorescence intensity was measured. This intensity correlates with the hybridization intensity. Two novel clones (referred to as P509S and P510S) were found to be over-expressed in prostate tumor and normal prostate and expressed at low levels in all other normal tissues tested (liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon). The determined cDNA sequences for P509S and P510S are provided in SEQ ID NO: 223 and 224, respectively. Comparison of these sequences with those in the gene bank as described above, revealed some homology to previously identified ESTs.

Example 2

DETERMINATION OF TISSUE SPECIFICITY OF PROSTATE TUMOR
POLYPEPTIDES

Using gene specific primers, mRNA expression levels for the representative prostate tumor polypeptides F1-16, H1-1, J1-17, L1-12, F1-12 and N1-1862 were examined in a variety of normal and tumor tissues using RT-PCR.

Briefly, total RNA was extracted from a variety of normal and tumor tissues using Trizol reagent as described above. First strand synthesis was carried out using 1-2 µg of total RNA with SuperScript II reverse transcriptase (BRL Life Technologies) at 42 °C for one hour. The cDNA was then amplified by PCR with gene-specific primers. To ensure the semi-quantitative nature of the RT-PCR, β-actin was used as an internal control for each of the tissues examined. First, serial dilutions of the first strand cDNAs were prepared and RT-PCR assays were performed using β-actin specific primers. A dilution was then chosen that enabled the linear range amplification of the β-actin template and which was sensitive enough to reflect the differences in the initial copy numbers. Using these conditions, the β-actin levels were determined for each reverse transcription reaction from each tissue. DNA contamination was minimized by DNase treatment and by assuring a negative PCR result when using first strand cDNA that was prepared without adding reverse transcriptase.

mRNA Expression levels were examined in four different types of tumor tissue (prostate tumor from 2 patients, breast tumor from 3 patients, colon tumor, lung tumor), and sixteen different normal tissues, including prostate, colon, kidney, liver, lung, ovary, pancreas, skeletal muscle, skin, stomach, testes, bone marrow and brain. F1-16 was found to be expressed at high levels in prostate tumor tissue, colon tumor and normal prostate, and at lower levels in normal liver, skin and testes, with expression being undetectable in the other tissues examined. H1-1 was found to be expressed at high levels in prostate tumor, lung tumor, breast tumor, normal prostate, normal colon and normal brain, at much lower levels in normal lung, pancreas, skeletal muscle, skin, small intestine, bone marrow, and was not detected in the other tissues tested. J1-17 and L1-12 appear to be specifically over-expressed in prostate, with both genes being expressed at high levels in

prostate tumor and normal prostate but at low to undetectable levels in all the other tissues examined. N1-1862 was found to be over-expressed in 60% of prostate tumors and detectable in normal colon and kidney. The RT-PCR results thus indicate that F1-16, H1-1, J1-17, N1-1862 and L1-12 are either prostate specific or are expressed at significantly elevated levels in prostate.

Further RT-PCR studies showed that F1-12 is over-expressed in 60% of prostate tumors, detectable in normal kidney but not detectable in all other tissues tested. Similarly, R1-2330 was shown to be over-expressed in 40% of prostate tumors, detectable in normal kidney and liver, but not detectable in all other tissues tested. U1-3064 was found to be over-expressed in 60% of prostate tumors, and also expressed in breast and colon tumors, but was not detectable in normal tissues.

RT-PCR characterization of R1-2330, U1-3064 and 1D-4279 showed that these three antigens are over-expressed in prostate and/or prostate tumors.

Northern analysis with four prostate tumors, two normal prostate samples, two BPH prostates, and normal colon, kidney, liver, lung, pancreas, skeletal muscle, brain, stomach, testes, small intestine and bone marrow, showed that L1-12 is over-expressed in prostate tumors and normal prostate, while being undetectable in other normal tissues tested. J1-17 was detected in two prostate tumors and not in the other tissues tested. N1-1862 was found to be over-expressed in three prostate tumors and to be expressed in normal prostate, colon and kidney, but not in other tissues tested. F1-12 was found to be highly expressed in two prostate tumors and to be undetectable in all other tissues tested.

The micro-array technology described above was used to determine the expression levels of representative antigens described herein in prostate tumor, breast tumor and the following normal tissues: prostate, liver, pancreas, skin, bone marrow, brain, breast, adrenal gland, bladder, testes, salivary gland, large intestine, kidney, ovary, lung, spinal cord, skeletal muscle and colon. L1-12 was found to be over-expressed in normal prostate and prostate tumor, with some expression being detected in normal skeletal muscle. Both J1-12 and F1-12 were found to be over-expressed in prostate tumor, with expression being lower or undetectable in all other tissues tested. N1-1862 was found to be expressed at high levels in prostate tumor and normal prostate, and at low levels in normal large intestine and normal

colon, with expression being undetectable in all other tissues tested. R1-2330 was found to be over-expressed in prostate tumor and normal prostate, and to be expressed at lower levels in all other tissues tested. 1D-4279 was found to be over-expressed in prostate tumor and normal prostate, expressed at lower levels in normal spinal cord, and to be undetectable in all other tissues tested.

Example 3

ISOLATION AND CHARACTERIZATION OF PROSTATE TUMOR POLYPEPTIDES BY PCR-BASED SUBTRACTION

A cDNA subtraction library, containing cDNA from normal prostate subtracted with ten other normal tissue cDNAs (brain, heart, kidney, liver, lung, ovary, placenta, skeletal muscle, spleen and thymus) and then submitted to a first round of PCR amplification, was purchased from Clontech. This library was subjected to a second round of PCR amplification, following the manufacturer's protocol. The resulting cDNA fragments were subcloned into the vector pT7 Blue T-vector (Novagen, Madison, WI) and transformed into XL-1 Blue MRF' *E. coli* (Stratagene). DNA was isolated from independent clones and sequenced using a Perkin Elmer/Applied Biosystems Division Automated Sequencer Model 373A.

Fifty-nine positive clones were sequenced. Comparison of the DNA sequences of these clones with those in the gene bank, as described above, revealed no significant homologies to 25 of these clones, hereinafter referred to as P5, P8, P9, P18, P20, P30, P34, P36, P38, P39, P42, P49, P50, P53, P55, P60, P64, P65, P73, P75, P76, P79 and P84. The determined cDNA sequences for these clones are provided in SEQ ID NO:41-45, 47-52 and 54-65, respectively. P29, P47, P68, P80 and P82 (SEQ ID NO:46, 53 and 66-68, respectively) were found to show some degree of homology to previously identified DNA sequences. To the best of the inventors' knowledge, none of these sequences have been previously shown to be present in prostate.

Further studies using the PCR-based methodology described above resulted in the isolation of more than 180 additional clones, of which 23 clones were found to show no

significant homologies to known sequences. The determined cDNA sequences for these clones are provided in SEQ ID NO: 115-123, 127, 131, 137, 145, 147-151, 153, 156-158 and 160. Twenty-three clones (SEQ ID NO: 124-126, 128-130, 132-136, 138-144, 146, 152, 154, 155 and 159) were found to show some homology to previously identified ESTs. An additional ten clones (SEQ ID NO: 161-170) were found to have some degree of homology to known genes. An additional clone, referred to as P703, was found to have five splice variants. The determined DNA sequence for the variants referred to as DE1, DE13 and DE14 are provided in SEQ ID NOS: 171, 175 and 177, respectively, with the corresponding predicted amino acid sequences being provided in SEQ ID NO: 172, 176 and 178, respectively. The DNA sequences for the splice variants referred to as DE2 and DE6 are provided in SEQ ID NOS: 173 and 174, respectively.

mRNA Expression levels for representative clones in tumor tissues (prostate (n=5), breast (n=2), colon and lung) normal tissues (prostate (n=5), colon, kidney, liver, lung (n=2), ovary (n=2), skeletal muscle, skin, stomach, small intestine and brain), and activated and non-activated PBMC was determined by RT-PCT as described above. Expression was examined in one sample of each tissue type unless otherwise indicated.

P9 was found to be highly expressed in normal prostate and prostate tumor compared to all normal tissues tested except for normal colon which showed comparable expression. P20 was found to be highly expressed in normal prostate and prostate tumor, compared to all twelve normal tissues tested. A modest increase in expression of P20 in breast tumor (n=2), colon tumor and lung tumor was seen compared to all normal tissues except lung (1 of 2). Increased expression of P18 was found in normal prostate, prostate tumor and breast tumor compared to other normal tissues except lung and stomach. A modest increase in expression of P5 was observed in normal prostate compared to most other normal tissues. However, some elevated expression was seen in normal lung and PBMC. Elevated expression of P5 was also observed in prostate tumors (2 of 5), breast tumor and one lung tumor sample. For P30, similar expression levels were seen in normal prostate and prostate tumor, compared to six of twelve other normal tissues tested. Increased expression was seen in breast tumors, one lung tumor sample and one colon tumor sample, and also in normal PBMC. P29 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5

of 5) compared to the majority of normal tissues. However, substantial expression of P29 was observed in normal colon and normal lung (2 of 2). P80 was found to be over-expressed in prostate tumor (5 of 5) and normal prostate (5 of 5) compared to all other normal tissues tested, with increased expression also being seen in colon tumor.

Further studies using the above methodology resulted in the isolation of twelve additional clones, hereinafter referred to as 10-d8, 10-h10, 11-c8, 7-g6, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3, 8-h11, g-f12 and g-f3. The determined DNA sequences for 10-d8, 10-h10, 11-c8, 8-d4, 8-d9, 8-h11, g-f12 and g-f3 are provided in SEQ ID NO: 207, 208, 209, 216, 217, 220, 221 and 222, respectively. The determined forward and reverse DNA sequences for 7-g6, 8-b5, 8-b6 and 8-g3 are provided in SEQ ID NO: 210 and 211; 212 and 213; 214 and 215; and 218 and 219, respectively. Comparison of these sequences with those in the gene bank revealed no significant homologies to the sequences of 7-g6 and g-f3. The clones 10-d8, 11-c8 and 8-h11 were found to show some homology to previously isolated ESTs, while 10-h10, 8-b5, 8-b6, 8-d4, 8-d9, 8-g3 and g-f12 were found to show some homology to previously identified genes.

Example 4

SYNTHESIS OF POLYPEPTIDES

Polypeptides may be synthesized on a Perkin Elmer/Applied Biosystems 430A peptide synthesizer using Fmoc chemistry with HPTU (O-Benzotriazole-N,N,N',N'-tetramethyluronium hexafluorophosphate) activation. A Gly-Cys-Gly sequence may be attached to the amino terminus of the peptide to provide a method of conjugation, binding to an immobilized surface, or labeling of the peptide. Cleavage of the peptides from the solid support may be carried out using the following cleavage mixture: trifluoroacetic acid:ethanedithiol:thioanisole:water:phenol (40:1:2:2:3). After cleaving for 2 hours, the peptides may be precipitated in cold methyl-t-butyl-ether. The peptide pellets may then be dissolved in water containing 0.1% trifluoroacetic acid (TFA) and lyophilized prior to purification by C18 reverse phase HPLC. A gradient of 0%-60% acetonitrile (containing 0.1% TFA) in water (containing 0.1% TFA) may be used to elute the peptides. Following

lyophilization of the pure fractions, the peptides may be characterized using electrospray or other types of mass spectrometry and by amino acid analysis.

From the foregoing, it will be appreciated that, although specific embodiments of the invention have been described herein for the purposes of illustration, various modifications may be made without deviating from the spirit and scope of the invention.

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: Xu, Jiangchun
Dillin, Davin C.

(ii) TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY OF PROSTATE CANCER
AND METHODS FOR THEIR USE

(iii) NUMBER OF SEQUENCES: 224

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: SEED and BERRY LLP
(B) STREET: 6300 Columbia Center, 701 Fifth Avenue
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98104

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE: 23-FEB-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Maki, David J.
(B) REGISTRATION NUMBER: 31,392
(C) REFERENCE/DOCKET NUMBER: 210121.427C3

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (206) 622-4900
(B) TELEFAX: (206) 682-6031

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 814 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

TTTTTTTTTT	TTTTTCACAG	TATAACAGCT	CTTTATTCT	GTGAGTTCTA	CTAGGAAATC	60
ATCAAATCTG	AGGGTTGTCT	GGAGGACTTC	AATAACACCTC	CCCCCATAGT	GAATCAGCTT	120
CCAGGGGGTC	CAGTCCCCTCT	CCTTACTTCA	TCCCCATCCC	ATGCCAAAGG	AAGACCCTCC	180
CTCCTTGGCT	CACAGCCTTC	TCTAGGCTTC	CCAGTGCCCTC	CAGGACAGAG	TGGGTTATGT	240
TTTCAGCTCC	ATCCTTGCTG	TGAGTGTCTG	GTGCGTTGTG	CCTCCAGCTT	CTGCTCAGTG	300
CTTCATGGAC	AGTGTCCAGC	ACATGTCACT	CTCCACTCTC	TCAGTGTGGA	TCCACTAGTT	360
CTAGAGCGGC	CGCCACCGCG	GTGGAGCTCC	AGCTTTGTT	CCCTTTAGTG	AGGGTTAATT	420

GCGCGCTTGG CGTAATCATG GTCATAACTG TTTCCGTGT GAAATTGTTA TCCGCTCACA	480
ATTCACACA ACATACGAGC CGGAAGCATA AAGTGAAAG CCTGGGGTGC CTAATGAGTG	540
ANCTAACTCA CATTAAATTC GTTGCCCTCA CTGNCCGCTT TCCAGTCNGG AAAACTGTCG	600
TGCCAGCTGC ATTAATGAAT CGGCCAACGC NCAGGGAAAAA CGGGTTTGCG TTTGGGGGC	660
TCTTCCGCTT CTCGCTCACT NANTCCTGCG CTGGCTCNNTT CGGCTGCAGG GAACGGTATC	720
ACTCTCTAAA GGNGGTATTA CGGTTATCCN NAAATCNGGG GATAACCNGG AAAAAANTTT	780
AACAAAAGGG CANCAAAGGG CNGAAACGTA AAAA	814

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 816 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

ACAGAAATGT TGGATGGTGG AGCACCTTTC TATAAGACTT ACAGGGACAGC AGATGGGGAA	60
TTCATGGCTG TTGGAGCAAT AGAACCCCCAG TTCTACGAGC TGCTGATCAA AGGACTTGGA	120
CTAAAGTCTG ATGAACCTCC CAATCAGATG AGCATGGATG ATTGGCCAGA AATGAAGAAG	180
AAGTTGCAG ATGTATTTCG AAAGAAGACG AAGGCAGAGT GGTGTCAAAT CTTTGACGGC	240
ACAGATGCCT GTGTGACTCC GGTCTGACT TTTGAGGAGG TTGTTCATCA TGATCACAAAC	300
AAGGAACGGG GCTCGTTTAT CACCAGTGAG GAGCAGGAGC TGAGCCCCCG CCCTGCACCT	360
CTGCTGTTAA ACACCCCAGC CATCCCTTCT TTCAAAAGGG ATCCACTAGT TCTAGAAGCG	420
GCCGCCACCG CGGTGGAGCT CCAGCTTTG TTCCCTTTAG TGAGGGTTAA TTGCGCGCTT	480
GGCTAATCA TGGTCATAGC TGGTCTGT GTGAAATTGT TATCCGCTCA CAATTCCCCC	540
AACATACGAG CGGAAACATA AAGTGTAAAG CCTGGGGTGC CTAATGANTG AGCTAACTCN	600
CATTAATTGC GTTGCCTCA CTGCCCCCTT TCCAGTCGGG AAAACTGTCG TGCCACTGCN	660
TTTGTGAAATC NGCCACCCCCC CGGGAAAAGG CGGTGCNTT TTGGGCCTCT TCCGCTTCC	720
TCGCTCATTC ATCCTNGCNC CGGTCTTCG GCTGCGGNGA ACGGTTCACT CCTCAAAGGC	780
GGTNTNCCGG TTATCCCCAA ACNNGGGATA CCCNGA	816

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 773 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CTTTTGAAAG AAGGGATGGC TGGGGTGTAA AACAGCAGAG GTGCAGGGCG GGGGCTCACG	60
TCTCTGCTCCT CACTGGTGAT AAACGAGCCC CGTTCCTGT TGTGATCATG ATGAACAAACC	120
TCCCTAAAGAAG TCAGAACCGG AGTCACACAG GCATCTGTGC CGTCAAAGAT TTGACACAC	180
TCTGCTTCG TCTTCTTGC AAATACATCT GCAAACCTCT TCTTCATTTC TGCCAATCA	240
TCCATGCTCA TCTGATTGGG AAGTTCATCA GACTTTAGTC CANNTCCCTT GATCAGCAGC	300
TCGTAGAACT GGGGTTCTAT TGCTCCAACA GCCATGAATT CCCCCTCTGC TGTCTGTAA	360
GTCGTATAGA AAGGTGCTCC ACCATCCAAC ATGTTCTGTGTC CTCGAGGGGG GGGCCGGTAC	420
CCAATTCGCC CTATANTGAG TCGTATTACG CGCGCTCACT GGCGCTCGTT TTACAACGTC	480
GTGACTGGGA AAACCCCTGGG CGTACCAAC TTAATGCGCT TGCAGCACAT CCCCCCTTCG	540
CCAGCTGGGC GTAATANCGA AAAGGCCGC ACCGATGCGC CTTCCAACAG TTGCGCACCT	600
GAATGGNAA ATGGGACCCC CCTGTTACCG CGCATTNAAC CCCCAGCNGGG TTTNGTTGTT	660
ACCCCCACNT NNACCGCTTA CACTTGCCTA GCGCCTTANC GCGCGCTCCC TTTNCCTTT	720
CTTCCCTTCC TTTCNCCCN CTTTCCCCCG GGGTTTCCCC CNTCAAACCC CNA	773

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 828 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CCTCCTGAGT	CCTACTGACC	TGTGCTTCT	GGTGTGGAGT	CCAGGGCTGC	TAGGAAAAGG	60
AATGGGCAGA	CACAGGTGTA	TGCCAATGTT	TCTGAAATGG	GTATAATTTC	GTCCTCTCCT	120
TCGGAACACT	GGCTGTCCT	GAAGACTTCT	CGCTCAGTTT	CAGTGAGGAC	ACACACAAAG	180
ACGTGGGTGA	CCATGTTGTT	TGTGGGGTGC	AGACATGGGA	GGGGTGGGGC	CCACCCCTGGA	240
AGAGTGGACA	GTGACACAAG	GTGGACACTC	TCTACAGATC	ACTGAGGATA	AGCTGGAGCC	300
ACAATGCATG	AGGCACACAC	ACAGCAAGGA	TGACNCTGTA	AACATAGCCC	ACGCTGTCCT	360
GNGGGCACTG	GGAAGCCTAN	ATNAGGCCGT	GAGCANAAAG	AAGGGGAGGA	TCCACTAGTT	420
CTANAGCGGC	CGCCACCGCG	GTGGANCTCC	ANCTTTGTT	CCCTTTAGTC	AGGGTTAATT	480
GCGCGCTTGG	CNTAACATG	GTCATANCTN	TTTCTGTGT	GAAATTGTTA	TCCGCTCAC	540
ATTCCACACA	ACATACGANC	CGGAAACATA	AANTGTAAAC	CTGGGGTGCC	TAATGANTGA	600
CTAACTCACA	TTAATTGCGT	TGCGCTCACT	GCCCCCTTTC	CAATCNGAA	ACCTGTCTG	660
CCNCTTGCAT	TNATGAATCN	GCCAACCCCC	GGGGAAAAGC	GTTCGCGTTT	TGGGCGCTCT	720
TCCGCTTCCCT	CNCTCANTTA	NTCCCTNCNC	TCGGTCATTC	CGGCTGCNGC	AAACCGGTT	780
ACCNCCCTCCA	AAGGGGGTAT	TCCGGTTCC	CCNAATCCGG	GGANANCC		828

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 834 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TTTTTTTTTT	TTTTTACTGA	TAGATGGAAT	TTATTAAGCT	TTTCACATGT	GATAGCACAT	60
AGTTTTAATT	GCATCCAAAG	TACTAACAAA	AACTCTAGCA	ATCAAGAATG	GCAGCATGTT	120
ATTTTATAAC	AATCAACACC	TGTGGCTTTT	AAAATTGGT	TTTCATAAGA	TAATTATAC	180
TGAAGTAAAT	CTAGCCATGC	TTTTAAAAAA	TGCTTTAGGT	CACTCCAAGC	TTGGCAGTTA	240
ACATTTGGCA	TAAACAATAA	AAAAACAAATC	ACAATTAAAT	AAATAACAAA	TACAACATTG	300
TAGGCCATAA	TCATATACAG	TATAAGGAAA	AGGTGGTAGT	GTTGAGTAAG	CAGTTATTAG	360
AATAGAACAT	CTTGGCCTCT	ATGCAAATAT	GTCTAGACAC	TTTGATTCA	TCAGCCCTGA	420
CATTCACTT	TCAAAGTAGG	AGACAGGTTC	TACAGTATCA	TTTACAGTT	TCCAACACAT	480
TGAAAACAAG	TAGAAAATGA	TGAGTTGATT	TTTATTAATG	CATTACATCC	TCAAGAGTTA	540
TCACCAACCC	CTCAGTTATA	AAAAATTTC	AAGTTATATT	AGTCATATAA	CTTGGTGTGC	600
TTATTTTAAA	TTAGTGCTAA	ATGGATTAAG	TGAAGACAAAC	ATGGTCCCC	TAATGTGATT	660
GATATTGGTC	ATTTTTACCA	GCTTCTAAAT	CTNAACTTTC	AGGTTTTGA	ACTGGAACAT	720
TGNATNACAG	TGTTCCANAG	TTNCAACCTA	CTGGAACATT	ACAGTGTGCT	TGATTCAAAA	780
TGTTATTTG	TTAAAATTAA	AATTTAAC	TGGTGGAAAA	ATAATTGAA	ATNA	834

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

TTTTTTTTTT TTTTTTTTTT AAGACCTCA TCAATAGATG GAGACATACA GAAATAGTCA	60
AACACATCT ACAAAATGCC AGTATCAGGC GGCGGCTTCG AAGCCAAAGT GATGTTTGA	120
TCTAAAGTGA AATATTAGTT GGCGGATGAA GCAGATAGTG AGGAAAGTTG AGCCAATAAT	180
GACGTGAAGT CCGTGGAAAGC CTGTGGCTAC AAAAATGTT GAGCCGTAGA TGCCGTGGA	240
AATGGTGAAG GGAGACTCGA AGTACTCTGA GGCTGTAGG AGGGTAAAAT AGAGACCCAG	300
TAAAAATTGTA ATAAGCAGTG CTTGAATTAT TTGGTTTCGG TTGTTTCTA TTAGACTATG	360
GTGAGCTAG GTGATTGATA CTCCGTATGC GAGTAATACG GATGTGTTTA GGAGTGGGAC	420
TTCTAGGGGA TTTAGCGGGG TGATGCCTGT TGGGGCCAG TGCCCTCCTA GTTGGGGGTT	480
AGGGGCTAGG CTGGAGTGGT AAAAGGCTCA GAAAATCCT GCGAAGAAAA AAACCTCTGA	540
GTTAATAAAT AGGATTATCC CGTATCGAAG GCCTTTTGG ACAGGTGGTG TGTGGTGGCC	600
TTGGTATGTG CTTTCTCGTG TTACATCGCG CCATCATGGG TATATGGTTA GTGTGTTGGG	660
TTANTANGGC CTANTATGAA GAACTTTGG ANTGAATTA AATCAATNGC TTGGCCGGAA	720
GTCATTANGA NGGCTNAAAA GGCCCTGTTA NGGGCTGGG CTNGGTTTA CCCNACCCAT	780
GGAATNCNCC CCCCGGACNA NTGNATCCCT ATTCTTAA	818

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 817 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

TTTTTTTTTT TTTTTTTTTT TGGCTCTAGA GGGGGTAGAG GGGGTGCTAT AGGGTAATA	60
CGGGCCCTAT TTCAAAGATT TTTAGGGAA TTAATTCTAG GACGATGGGT ATGAAACTGT	120
GGTTTGCTCC ACAGATTCA GAGCATTGAC CGTAGTATAC CCCCAGTCGT GTAGCGGTGA	180
AAGTGGTTG GTTAGACGT CCGGAATTG CATCTGTTT TAAGCCTAAAT GTGGGGACAG	240
CTCATGAGTG CAAGACGTCT TGTGATGTAA TTATTATACN AATGGGGCT TCAATCGGA	300
GTACTACTCG ATTGTCAACG TCAAGGAGTC GCAGGTCGCC TGGTTCTAGG AATAATGGG	360
GAAGTATGTA GGAATTGAAG ATTAATCCGC CGTAGTCGGT GTTCTCCTAG GTTCAATACC	420
ATTGGTGGCC AATTGATTG ATGGTAAGGG GAGGGATCGT TGAACTCGTC TGTTATGTAA	480
AGGATNCNTT NGGGATGGGA AGGCNATNAAG GAACTANGGA TNAATGGCGG GCANGATATT	540
TCAAACNGTC TCTANTTCCT GAAACGCTG AAATGTTAAT AANAATTAAN TTNNGTTATT	600
GAATNTTNNNG GAAAAGGGCT TACAGGACTA GAAACCAAAT ANGAAAANTA ATNNTAANGG	660
CNTTATCNTN AAAGGTNATA ACCNCCTCA TNATCCCACC CAATNGNATT CCCCCACNCNN	720
ACNATTGGAT NCCCCANTTC CANAAANGGC CNCCCCCGG TGNANNCCNC CTTTTGTTCC	780
CTTNANTGAN GGTTATTNCNC CCCTNGCNTT ATCANCC	817

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 799 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CATTTCCGGG TTTACTTTCT AAGGAAAGCC GAGCGGAAGC TGCTAACGTG GGAATCGGTG	60
CATAAGGAGA ACTTTCTGCT GGCACCGCGT AGGGACAAGC GGGAGAGCGA CTCCGAGCGT	120

CTGAAGCGCA CGTCCCAGAA GGTGGACTTG GCACTGAAAC AGCTGGGACA CATCCGCGAG	180
TACGAACAGC GCCTGAAAGT GCTGGAGCGG GAGGTCCAGC AGTGTAGCCG CGTCCTGGG	240
TGGGTGGCCG ANGCCTGANC CGCTCTGCCCT TGCTGCCCCC ANGTGGGCCG CCACCCCCCTG	300
ACCTGCCTGG GTCCAAACAC TGAGCCCTGC TGCGGACTT CAAGGANAAC CCCCACANGG	360
GGATTTTGC CCTANANTAA GGCTCATCTG GGCGCTGGCC CCCCCCACCTG GTTGGCCTTG	420
TCTTTGANGT GAGCCCCATG TCCATCTGGG CCACTGTCNG GACCACCTT NGGGAGTGT	480
CTCCTTACAA CCACANNATG CCCGGCTCCT CCCGGAAACC ANTCCCANCC TGNGAAGGAT	540
CAAGNCCTGN ATCCACTNNT NCTANAACCG GCCNCCNCCG CNGTGGAACCC CNCCCTNTGT	600
TCCTTTTCNT TNAGGGTTAA TNNGCCTTG GCCTTNCCAN NGTCCTNCNC NTNTTCCNNT	660
GTNAAATTG TTANGCNCCC NCCNNTCCN CNNNCNCAN CCCGACCCNN ANNTNNNANN	720
NCCTGGGGGT NCCNNCNGAT TGACCCNNCC NCCCTNTANT TGCNTTNGGG NNCNNTGCC	780
CTTCCCTCT NGGGANNCG	799

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 801 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

ACGCCTTGAT CCTCCCAGGC TGGGACTGGT TCTGGGAGGA GCCGGGCATG CTGTGGTTTG	60
TAANGATGAC ACTCCCAAAG GTGGTCTCTGA CAGTGGCCCA GATGGACATG GGGCTCACCT	120
CAAGGACAAG GCCACCAGGT GCGGGGGCCG AAGCCCACAT GATCCTTACT CTATGAGCAA	180
AATCCCTGTG GGGGGCTTCT CCTTGAAGTC CGCCANCAGG GCTCAGTCTT TGGACCCANG	240
CAGGTCTGGG GTTGTNGNC CAACTGGGG CCNCAACGCA AAANGGCNCA GGGCCTCNGN	300
CACCCATCCC ANGACGCGC TACACTNCTG GACCTCCNC TCCACCACTT TCATGCGCTG	360
TTCTNACCCG CGNATNTGTC CCANCTGTTT CNGTGCNAC TCCANCTTCT NGGACGTGCG	420
CTACATACGC CGGGANTCNC NCTCCCCTT TGTCCTATC CACGTNCCAN CAACAAATT	480
CNCCNTANTG CACCNATTCC CACNTTNNC AGNTTCCNC NNCGNGCTTC CTTNTAAAAG	540
GGTTGANCCC CGGAAATNC CCCAAAGGGG GGGGGCCNGG TACCCAACTN CCCCCCTNATA	600
GCTGAANTCC CCATNACCN GNCTCNATGG ANCCNTCCNT TTTAANNACN TTCTNAACTT	660
GGGAANANCC CTCGNCCNTN CCCCCNTTAA TCCCNCCCTTG CNANGNNCNT CCCCCNNNTCC	720
NCCNNNTNG GCNTNTNANN CNAAAAAGGC CNNNNANCAA TCTCCTNNCN CCTCANTTCG	780
CCANCCCTCG AAATCGGCCN C	801

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 789 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

CAGTCTATNT GGCCAGTGTG GCAGCTTCC CTGTGGCTGC CGGTGCCACA TGCCTGTCCC	60
ACAGTGTGGC CGTGGTGACA GCTTCAGCCG CCCTCACCGG GTTCACCTTC TCAGCCCTGC	120
AGATCCTGCC CTACACACTG GCCTCCCTCT ACCACCGGGA GAAGCAGGTG TTCCCTGCCA	180
AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGGACAG CCTGATGACC AGCTTCCCTGC	240
CAGGCCCTAA GCCTGGAGCT CCCTTCCCTA ATGGACACGT GGGTGTGGA GGCAGTGGCC	300
TGCTCCCACC TCCACCCGGG CTCTGCGGGG CCTCTGCCTG TGATGTCTCC GTACGTGTGG	360
TGGTGGGTGA GCCCACCAGAN GCCAGGGTGG TTCCGGGCCG GGGCATCTGC CTGGACCTCG	420
CCATCCTGGA TAGTGCTTCC TGCTGTCCCA NGTGGCCCCA TCCCTGTTA TGGGCTCCAT	480
TGTCCAGCTC AGCCAGTCTG TCACTGCCTA TATGGTGTCT GCCGCAGGCC TGGGTCTGGT	540

CCCATTTACT TTGCTACACA GGTANTATTT GACAAGAACG ANTTGGCCAA ATACTCAGCG	600
TTAAAAAATT CCAGCAACAT TGGGGGTGGA AGGCCTGCCT CACTGGGTCC AACTCCCCGC	660
TCTCTTAAAC CCCATGGGC TGCCGGCTTG GCCCCAATT TCTGTTGCTG CCAAANTNAT	720
GTGGCTCTCT GCTGCCACCT GTTGCTGGCT GAAGTGCNTA CNGCNCANCT NGGGGGGTNG	780
GGNGTTCCC	789

(2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 772 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CCCACCCCTAC CCAAATATTA GACACCAACA CAGAAAAGCT AGCAATGGAT TCCCTTCTAC	60
TTTGTAAAT AAATAAGTTA AATATTAAA TGCCCTGTTC TCTGTGATGG CAACAGAAGG	120
ACCAACAGGC CACATCCTGA TAAAAGGTTA GAGGGGGGTG GATCAGCAAA AAGACAGTGC	180
TGTGGGCTGA GGGGACCTGG TTCTTGTGTG TTGCCCTCA GGACTCTTCC CCTACAAATA	240
ACTTTCATAT GTTCAAATCC CATGGAGGAG TGTTTCATCC TAGAAACTCC CATGCAAGAG	300
CTACATTAAA CGAAGCTGCA CGTTAAAGGGG CTTANAGATG GGAAACCAGG TGACTGAGTT	360
TATTCAAGCTC CCAAAAACCC TTCTCTAGGT GTGTCTCAAC TAGGAGGCTA GCTGTTAAC	420
CTGAGCCTGG GTAATCCACC TGCAGAGTCC CCGCATTCCA GTGCATGGAA CCCTTCTGGC	480
CTCCCTGTAT AAGTCCAGAC TGAAACCCCCC TTGGAAGGNC TCCAGTCAGG CAGCCCTANA	540
AACTGGGAA AAAAGAAAAG GACGCCCAN CCCCCAGCTG TGCANCTACG CACCTCAACA	600
GCACAGGGTG GCAGCAAAAA ACCACTTTA CTTTGGCACA AACAAAAACT NGGGGGGCA	660
ACCCCGGCAC CCCNANGGG GTAACAGGA ANCNGGGNA CNTGGAACCC AATTNAGGCA	720
GGCCCNCCAC CCCNAATNTT GCTGGAAAT TTTCTCCC CTAAATTNTT TC	772

(2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 751 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

GCCCCAATTG CAGCTGCCAC ACCACCCACG GTGACTGCAT TAGTTCGGAT GTCATACAAA	60
AGCTGATTGA AGCAACCTTC TACTTTTGG TCGTGAGCCT TTGCTTGGT GCAGGTTCA	120
TTGGCTGTGT TGGTGACGTT GTCATTGCAA CAGAAATGGGG GAAAGGCCT GTTCTCTTG	180
AAGTANGGTG AGTCCCTAAA ATCCGTATAG TTGGTGAAGC CACAGCACTT GAGCCCTTC	240
ATGGTGGTGT TCCACACTTG AGTGAAGTCT TCCTGGGAAC CATAATCTTT CTTGATGGCA	300
GGCACTACCA GCAACGTCAAG GGAAGTGTG AGCCATTGTG GTGTACACCA AGGCGACAC	360
AGCAGCTGCN ACCTCAGCAA TGAAGATGAN GAGGANGATG AAGAAGAACG TCNCGAGGGC	420
ACACTTGCTC TCAGTCTTAN CACCATANCA GCCCNTGAAA ACCAANANCA AAGACCACNA	480
CNCCGGCTGC GATGAAGAAA TNACCCCNCG TTGACAAACT TGCATGGCAC TGGGANCCAC	540
AGTGGCCCNAA AAAATCTTCA AAAAGGATGC CCCATCNATT GACCCCCCAA ATGCCACTG	600
CCAACAGGGG CTGCCCCACN CNCNNAACGA TGANCCNATT GNACAAGATC TNCNTGGCT	660
TNATNAACNT GAACCCCTGCN TNGTGGCTCC TGTTCAGGNC CNNGGCCTGA CTTCTNAANN	720
AANGAACTCN GAAGNCCCCA CNGGGANANN G	751

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 729 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GAGCCAGGCG	TCCCTCTGCC	TGCCCCACTCA	GTGGCAACAC	CCGGGAGCTG	TTTTGTCCTT	60
TGTGGANCCT	CAGCAGTNCC	CTCTTTAGA	ACTCANTGCC	AAGANCCCTG	AAACAGGAGCC	120
ACCATGCAGT	GCTTCAGCTT	CATTAAGACC	ATGATGATCC	TCTTCAATT	GCTCATCTT	180
CTGTGTGGTG	CAGCCCTGTT	GGCAGTGGGC	ATCTGGGTGT	CAATCGATGG	GGCATCCTT	240
CTGAAGATCT	TCGGGCCACT	GTCGTCCAGT	GCCATGCAGT	TTGTCAACGT	GGGCTACTTC	300
CTCATCGCAG	CCGGCGTTGT	GGTCTTAGCT	CTAGGTTTCC	TGGGCTGCTA	TGGTGCTAAG	360
ACTGAGAGCA	AGTGTGCCCT	CGTGACGTC	TTCTTCATCC	TCCTCCTCAT	CTTCATTGCT	420
GAGGTTGCAA	TGCTGTGGTC	GCCTTGGTGT	ACACCACAAT	GGCTGAGCAC	TTCCTGACGT	480
TGCTGGTAAT	GCCTGCCATC	AANAAAAGAT	TATGGGTTCC	CAGGAANACT	TCACTCAAGT	540
GTTGGAACAC	CACCATGAAA	GGGCTCAAGT	GCTGTGGCTT	CNNCCAACTA	TACGGATT	600
GAAGANTCAC	CTACTTCAA	GAAAANAGTG	CCTTCCCCC	ATTCTGTTG	CAATTGACAA	660
ACGTCCCCAA	CACAGCCAAT	TGAAAACCTG	CACCCAACCC	AAANGGTCC	CCAACCANAA	720
ATTNAAGGG						729

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 816 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

TGCTCTTCCT	CAAAGTTGTT	CTTGTGCCA	TAACAAACCAC	CATAGGTAAA	GCGGGCGCAG	60
TGTCGCTGA	AGGGGTTGTA	GTACCAGCGC	GGGATGCTCT	CCTTGCAGAG	TCCTGTGTCT	120
GGCAGGTCCA	CGCAGTGCC	TTTGTCACTG	GGGAAATGGA	TGCCTGGAG	CTCGTCAAAG	180
CCACTCGTGT	ATTTTCACA	GGCAGCCTCG	TCCGACGCGT	CGGGGCAGTT	GGGGGTGTCT	240
TCACACTCCA	GGAAACTGTC	NATGCAGCAG	CCATTGCTGC	AGCGGAACTG	GGTGGGCTGA	300
CANGTGCCAG	AGCACACTGG	ATGGCGCCTT	TCCATGNAN	GGGCCCTGNG	GGAAAGTCCC	360
TGANCCCCAN	ANCTGCTCT	CAAANGCCC	ACCTGCACA	CCCCGACAGG	CTAGAATGGA	420
ATCTTCTTCC	CGAACAGGTAG	TTNTTCTTGT	TGCCCAANCC	ANCCCCNTAA	ACAAACTCTT	480
GCANATCTGC	TCCCGNGGGG	TCNTANTACC	ANCGTGGGAA	AAGAACCCCA	GGCNGCGAAC	540
CAANCTGTT	TGGATNCGAA	GCNATAATCT	NCTNTTCTGC	TTGGTGGACA	GCACCANTNA	600
CTGTNNANCT	TTAGNCCNTG	GTCCTCNTGG	GTTGNNCNTG	ACCTAATCN	CCNNNTCAACT	660
GGGACAAGGT	AANTNGCCNT	CCTTTNAATT	CCCNANCNTN	CCCCCTGGTT	TGGGGTTTTN	720
CNCNCTCCTA	CCCCAGAAAAN	NCCGTGTTCC	CCCCCAACTA	GGGGCCNAAA	CCNNNTNTTC	780
CACAACCCNT	CCCCACCCAC	GGGTTCNGNT	GGTTNG			816

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 783 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

CCAAGGCCTG	GGCAGGCATA	NACTTGAAGG	TACAACCCCA	GGAACCCCCTG	GTGCTGAAGG	60
ATGTGGAAAA	CACAGATTGG	CGCCTACTGC	GGGGTGACAC	GGATGTCAGG	GTAGAGAGGA	120
AAGACCCAAA	CCAGGTGGAA	CTGTGGGGAC	TCAAGGAANG	CACCTACCTG	TTCCAGCTGA	180
CAGTGA	CTCAGACCAC	CCAGAGGACA	CGGCCAACGT	CACAGTCACT	GTGCTGTCCA	240
CCAAGCAGAC	AGAAGACTAC	TGCCTCGCAT	CCAACAANGT	GGGTCGCTGC	CGGGGCTCTT	300
TCCCACGCTG	GTACTATGAC	CCCACGGAGC	AGATCTGCAA	GAGTTTCGTT	TATGGAGGCT	360
GCTTGGGCAA	CAAGAACAAAC	TACCTTCGGG	AAGAAGAGTG	CATTCTANCC	TGTCNGGGTG	420
TGCAAGGTGG	GCCTTGTANA	NGCANCTCTG	GGGCTCANGC	GACTTTCCCC	CAGGGCCCCCT	480
CCATGGAAAG	GCGCCATCCA	NTGTTCTCTG	GCACCTGTCA	GCCCACCCAG	TTCCGCTGCA	540
NCAATGGCTG	CTGCATCNAC	ANTTTCTCTNG	AATTGTGACA	ACACCCCCCA	NTGCCCCAA	600
CCCTCCCAAC	AAAGCTTCCC	TGTTNAAAA	TACNCCANTT	GGCTTTTNAC	AAACNCCCGG	660
CNCCTCCNTT	TTCCCCNNNT	AAACAAGGC	NCTNGCNNTT	GAAC TGCCCN	AAACCNNGAA	720
TCTNCCNNGG	AAAANTNCC	CCCCCTGGTT	CCTNNAANCC	CCTCCNCNAA	ANCTNCCCC	780
CCC						783

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 801 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GCCCCAATTC	CAGCTGCCAC	ACCACCCACG	GTGACTGCAT	TAGTTCGGAT	GTCATACAAA	60
AGCTGATTGA	AGCAACCCCTC	TACTTTTG	TCGTGAGCCT	TTTGCTTGGT	GCAGGTTTCA	120
TTGGCTGTGT	TGGTGACGTT	GTCATTGCAA	CAGAATGGGG	GAAAGGCAC	GTTCTCTTG	180
AAGTAGGGTG	AGTCCTCAA	ATCCGTATAG	TTGGTGAAAGC	CACAGCACTT	GAGCCCTTTC	240
ATGGTGGTGT	TCCACACTTG	AGTGAAGTCT	TCCCTGGAAAC	CATAATCTTT	CTTGATGGCA	300
GGCACTACCA	GCAACGTCAG	GAAGTGCTCA	GCCATTGTGG	TGTACACCAA	GGCGACCCACA	360
GCAGCTGCAA	CCTCAGCAAT	GAAGATGAGG	AGGAGGATGA	AGAAGAACGT	CNCGAGGGCA	420
CACTTGCTCT	CCGTCTTAGC	ACCATAGCAG	CCCANGAAAC	CAAGAGCAA	GACCACAAACG	480
CCNGCTGCGA	ATGAAAGAAA	NTACCCACGT	TGACAAACTG	CATGGCCACT	GGACGACAGT	540
TGGCCCGAAN	ATCTTCAGAA	AAGGGATGCC	CCATCGATTG	AACACCCANA	TGCCCACACTG	600
CNACAGGGCT	GCNCCNCNCN	AAAAGAATGA	GCCATTGAAAG	AAGGATCN	NTGGTCTTAA	660
TGAAGTGA	CCNTGCATGG	TGGCCCTGT	TCAGGGCTCT	TGGCAGTGAA	TTCTGANAAA	720
AAGGAACNGC	NTNAGCCCCC	CCAAANGANA	AAACACCCCC	GGGTGTTGCC	CTGAATTGGC	780
GGCCAAGGAN	CCCTGCCCN	G				801

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 740 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GTGAGAGCCA	GGCGTCCCTC	TGCCTGCCA	CTCAGTGGCA	ACACCCGGGA	GCTGTTTGT	60
CCTTTGTGGA	GCCTCAGCAG	TTCCCTCTT	CAGAACTCAC	TGCCAAGAGC	CCTGAACAGG	120
AGCCACCATG	CAGTGCTTCA	GCTTCATTAA	GACCATGATG	ATCCTCTTCA	ATTGCTCAT	180
CTTTCTGTGT	GGTGCAGCCC	TGTTGGCAGT	GGGCATCTGG	GTGCAATCG	ATGGGGCATC	240
CTTTCTGAAG	ATCTTCGGGC	CACTGTCGTC	CAGTGCCATG	CAGTTTGTCA	ACGTGGGCTA	300
CTTCCTCATC	GCAGCCGGCG	TTGTGGTCTT	TGCTCTTGGT	TTCCTGGGCT	GCTATGGTGC	360

TAAGACGGAG AGCAAGTGTG CCCTCGTGAC GTTCTTCITC ATCCCTCTCC TCATCTTCAT	420
TGCTGAAGTT GCAGCTGCTG TGGTCGCCCT GGTGTACACC ACAATGGCTG AACCATTCCCT	480
GACGTTGCTG GTANTGCCTG CCATCAANAA AGATATGGG TTCCCAGGAA AAATTCACTC	540
AANTNTGGAA CACCNCCATG AAAAGGGCTC CAATTCTGN TGGCTTCCCC AACTATAACCG	600
GAATTTGAA AGANTCNCCC TACTTCCAAA AAAAAAANANT TGCCCTTNCC CCCNTTCTGT	660
TGCAATGAAA ACNTCCAAN ACNGCCAATN AAAACCTGCC CNNNCNNAAA GGNTCNAAA	720
CAAAAAAANT NNAAGGGTTN	740

(2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 802 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCGCTGGTT CGCTGGTCCA GNGNAGCCAC GAAGCACGTC AGCATACACA GCCTCAATCA	60
CAAGGTCTTC CAGCTGCCGC ACATTACGCA GGGCAAGAGC CTCCAGCAAC ACTGCATATG	120
GGATACACTT TACTTTAGCA GCCAGGGTGA CAACTGAGAG GTGTCGAAGC TTATTCTTCT	180
GAGCCTCTGT TAGTGGAGGA AGATTCCGGG CTTCAGCTAA GTAGTCAGCG TATGTCCCAT	240
AAGCAAACAC TGTGAGCAGC CGGAAGGTAG AGGCAAAGTC ACTCTCAGCC AGCTCTCTAA	300
CATTGGGCAT GTCCAGCAGT TCTCCAAACA CGTAGACACC AGNGGCCTCC AGCACCTGAT	360
GGATGAGTGT GGCCAGCGCT GCCCCCTTGG CCGACTTGGC TAGGAGCAGA AATTGCTCCT	420
GGTCTCTGCCC TGTCACCTTC ACTTCCGCAC TCATCACTGC ACTGAGTGTG GGGGACTTGG	480
GCTCAGGATG TCCAGAGACG TGGTTCCGCC CCCTCNCTTA ATGACACCGN CCANNCAACC	540
GTCGGCTCCC GCCGANTGNG TTCGTCGTNC CTGGGTCAGG GTCTGCTGGC CNCTACTTGC	600
AANCTTCGTC NGGCCATGG AATTCAACNC ACCGGAACCTN GTANGATCCA CTNNTTCTAT	660
AACCGGNCGC CACCGCENNNT GGAACCTCCAC TCTTNTTNCC TTTACTTGAG GTTAAAGGTC	720
ACCCCTNNCG TTACCTTGGT CCAAACCNNTN CCNTGTGTG ANATNGTNAA TCNGGNCCNA	780
TNCCANCCNC ATANGAAGCC NG	802

(2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

CNAAGCTTCC AGGTNACGGG CGCGNAANCC TGACCCNAGG TANCANAANG CAGNCNGCGG	60
GAGCCCCACCG TCACGNNGNG GNNGTCTTAT NGGAGGGGGC GGAGCCACAT CNCTGGACNT	120
CNTGACCCCCA ACTCCCCNCC NCNCANTGCA GTGATGAGTG CAGAACTGAA GTGNACGTGG	180
CAGGAACCAA GANCAAANNC TGCTCCNNTC CAAGTCGGCN NAGGGGGCGG GGCTGGCCAC	240
GCNCATCCNT CNAGTGCTGN AAAGCCCCNN CCTGTCCTACT TGTTTGAGA ACNGCENNNGA	300
CATGCCCAAGN GTTANATAAAC NGGCNGAGAG TNANTTGCC TCTCCCTTCC GGCTGCGCAN	360
CGMGTNTGCT TAGNGGACAT AACCTGACTA CTTAACTGAA CCCNNGAATC TNCCNCCCT	420
CCACTAAGCT CAGAACAAAA AACCTCGACA CCACTCANTT GTCACCTGNC TGCTCAAGTA	480
AAAGTGTACCC CATNCCCAAT GTNTGCTNGA NGCTCTGNCC TGCNTTANGT TCGGTCTGG	540
GAAGACCTAT CAATTNAAGC TATGTTCTG ACTGCCCTT GCTCCCTGNA ACAANCNACC	600
CNNCNNTCCA AGGGGGGGNC GGCCCCCAAT CCCCCCAACC NTNAATTNAN TTTANCCCN	660
CCCCCNNGCC CGGCCTTTA CNANCNTCNN NNACNGGNA AAACCNNGC TTTNCCCAAC	720
NNAATCCNCC T	731

(2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 754 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

TTTTTTTTT	TTTTTTTTT	TAAAAACCC	CTCCATTNAA	TGNAAACTTC	CGAAATTGTC	60
CAACCCCCTC	NTCCAATNN	CCNTTCCGG	GNGGGGTTC	CAAACCCAAN	TTANNTTTGG	120
ANNTTAAATT	AAATNTNNNT	TGGNGGNNA	ANCCNAATGT	NANGAAAGTT	NAACCCANTA	180
TNANCTTNA	TNCCCTGGAAA	CCNGTGNNT	CCAAAATNT	TTAACCCCTTA	ANTCCCTCCG	240
AAATNGTTNA	NGGAAAACCC	AANTCTCNT	AAGGTTGTTT	GAAGGNTNAA	TNAAAANCCC	300
NNCCAATTGT	TTTTNGCCAC	GCCTGAATTA	ATTGGNTTCC	GNTGTTTCC	NTTAAAANAA	360
GGNNANCCCC	GGTTANTNAA	TCCCCCCNNC	CCCAATTATA	CCGANTTTTT	TTNGAATTGG	420
GANCCCNCGG	GAATTAACGG	GGNNNNNTCCC	TNTTGGGGGG	CNGGNNNCCC	CCCCNTCGGG	480
GGTNGGGNC	AGGNCNNAAT	TGTTTAAGGG	TCCGAAAAT	CCCTCCNAGA	AAAAAANCTC	540
CCAGGNTGAG	NNTNGGGTT	NCCCCCCCCC	CANGCCCCCT	CTCGNANAGT	TGGGGTTTGG	600
GGGGCCTGGG	ATTTTNTTTC	CCCTNTTNCC	TCCCCCCCCC	CCNGGGANAG	AGGTTNGNGT	660
TTTGNTCNNC	GGCCCCNCCN	AAGANCTTN	CCGANNTNAN	TTAAATCCNT	GCCTNGGCGA	720
AGTCCNTTGN	AGGGNTAAAN	GGCCCCCTNN	CGGG			754

(2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 755 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ATCANCCCAT	GACCCNAAC	NNGGGACCNC	TCANCCGGNC	NNNCNACCNC	CGGCCNATCA	60
NNGTNAGNNC	ACTNCNNTTN	NATCACNCCC	CNCCNACTAC	GCCCNANC	CNACGCNCTA	120
NNCANATNCC	ACTGANNCGG	CGANGTNGAN	NGAGAAANCT	NATACCANAG	NCACCAANACN	180
CCAGCTGTCC	NANAANGCCT	NNNATACNGG	NNNATCCAAT	NTGNANCTC	CNAAGTATTN	240
NNCNNCANAT	GATTTTCCTN	ANCCGATTAC	CCNTCCCCC	TANCCCTCC	CCCCAACNA	300
CGAAGGCNCT	GGNCCNAAGG	NNGCGNCNCC	CCGCTAGNTC	CCCNNAAGT	CNCNCNCTA	360
AACTCANCCN	NATTACNCGC	TTCNTGAGTA	TCACTCCCCG	AATCTCACCC	TACTCAACTC	420
AAAAANATCN	GATAACAAAT	AATNCAAGCC	TGNTTATNAC	ACTNTGACTG	GGTCTCTATT	480
TTAGNGGTCC	NTNAANCNTC	CTAATACTTC	CACTCTNCT	TCNCCAATT	CCNAANGGCT	540
CTTTCNGACA	GCATNTTTG	GTTCCCNNTT	GGGTCTTAN	NGAATTGCCC	TTCNTNGAAC	600
GGGCTCCTCT	TTTCCTTCGG	TTANCTTGGN	TCNNCCGGC	CAGTTATTAT	TTCCCNNTTT	660
AAATTCTNTNC	CNTTTTANTTT	TGGCNTTCNA	AACCCCGGC	CTTGAAAACG	CCCCCTGGT	720
AAAAGGTTGT	TTTGANAAAA	TTTTGTTTT	GTTCC			755

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 849 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

TTTTTTTTT TTTTTTANGTG TNGTCGTGCA GGTAGAGGCT TACTACAANT GTGAANACGT	60
ACGCTNGGAN TAANGCGACC CGANTTCTAG GANNNCNCCT AAAATCANAC TGTGAAGATN	120
ATCCTGNNA CGGAANGGTC ACCGGNNGAT NNTGCTAGGG TGNCCNCTCC CANNNCNTTN	180
CATAACTCNG NGGCCCTGCC CACCACCTTC GGCGGCCNG NGNCCGGGCC CGGGTCATTN	240
GNNTTAACCN CACTNNGCNA NCGGTTCCN NCCCCNNCNG ACCCNNGCGA TCCGGGGTNC	300
TCTGTCTTCC CCTGNAGNCN ANAAANTGGG CCNCGGNCCC CTTTACCCCT NNACAAAGCCA	360
CNGCCNTCTA NCCNCNGCCC CCCCTCCANT NNGGGGGACT GGCNANNGCT CCGTTNCTNG	420
NNACCCNNN GGGTNCCTCG GTTGTGANT CNACCGNANG CCANGGATTG CNAAGGAAGG	480
TGCGTTNTTG GCCCCTACCC TTCGCTNCGG NNCACCCCTTC CCGACNANGA NCCGCTCCG	540
CNCNNCGNNG CCTCNCTCG CAACACCCGC NCTCNTCNGT NC GGNNNNCCC CCCCACCCGC	600
NCCCTCNCNC NGNGNANCN CTCCNCCNCC GTCTCANNCA CCACCCCGCC CCGCCAGGCC	660
NTCACACN GGNNGACNNG NAGCNCNTC GCNCGGCN GCGNCNCCT CGCCNCNGAA	720
CTNCNTCNGG CCANTNNCGC TCAANCCNA CNAACGCCG CTGCGCGGCC CGNAGCGNCC	780
NCCTCCNCGA GTCCCTCCCGN CTTCCNACCC ANGNNTCCN CGAGGACACN NNACCCCGCC	840
NNCANGCGG	849

(2) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 872 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GCGCAAACTA TACTTCGCTC GNACTCGTGC GCCTCGCTNC TCTTTTCCTC CGCAACCAGT	60
TCTGACNANC CCGATTNGGC NGATATCNAN AAGNTCGANC AGTCCAAACT GANTAACACA	120
CACACNCNAN AGANAAATCC NCTGCTTCC ANAGTANACN ATTGAACNNG AGAACCCANGC	180
NGGCGAATCG TAATNAGGCG TGCGCCGCA ATNTGTCNCC GTTTATTNTN CCAGCNTCNC	240
CTNCCNACCC TACNTCTTCN NAGCTGTCNN ACCCCTNGTN CGNACCCCCC NAGGTCGGGA	300
TCGGGTTTNN NNTGACCGNG CNNCCCTCC CCCNTCCAT NACGANCCNC CCGCACCAACC	360
NANNGCNCGC NCCCCGNNCT CTTCGCCNCC CTGTCCTNTN CCCCTGTNGC CTGGCNCNGN	420
ACCGCATTGA CCCTCGCCNN CTNCNNNGAA NCGNANACGT CCGGGTTGNN ANNANCGCTG	480
TGGGNNNGCG TCTGCNCCGC GTTCCTTCCN NCNNCTTCCA CCATCTTCNT TACNGGGTCT	540
CCNCGCCNTC TCNNNCACNC CCTGGGACGC TNTCCTNTGC CCCCTTNAC TCCCCCCCTT	600
CGNCGTGNCC CGNCCCCACC NTCAATTNA NACGNTCTTC ACAANNNCCT GGNTNNCTCC	660
CNANCNGNCN GTCANCCNAG GGAAGGGNGG GGNNCNNNT NTTGACGTTG NGGNGANGTC	720
CGAANANTCC TCNCCNTCAN CNCTACCCCT CGGGCGNNCT CTCNGTTNCC AACTTANCAA	780
NTCTCCCCCG NGNGCNCNTC TCAGCCTCNC CCNCCCNCT CTCTGCANTG TNCTCTGCTC	840
TNACCNNTAC GANTNTTCGN CNCCCTTTT CC	872

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 815 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

GCATGCAAGC TTGAGTATTTC TATAGNGTCA CCTAAATANC TTGGCNTAAT CATGGTCNTA	60
NCTGNCTTCC TGTGTCAAAT GTATACNAAN TANATATGAA TCTNATNTGA CAAGANNGTA	120

TCNTNCATTA	GTAACAANTG	TNNTGTCCAT	CCTGTCNGAN	CANATTCCCA	TNNATTNCGN	180
CGCATTNCN	GCNCANTATN	TAATNGGAA	NTCNNTNNN	NCACCNNCAT	CTATCNTNCC	240
GCNCCTGAC	TGGNAGAGAT	GGATNAMITC	TNNNTGACC	NACATGTTCA	TCTTGGATTN	300
AANANCCCC	CGCNGNCCAC	CGGTTNGNNG	CNAGCCNNTC	CCAAGACCTC	CTGTGGAGGT	360
AACCTCGTC	AGANNCATCA	AACNTGGAA	ACCCGCNNCC	ANGTNNAAGT	NGNNNCANAN	420
GATCCCGTCC	AGGNTTNACC	ATCCCTTNC	AGCGCCCCCT	TTNGTGCCTT	ANAGNGNAGC	480
GTGTCCNANC	CNCTCAACAT	GANACGCGCC	AGNCANCCG	CAATTNGGCA	CAATGTCGN	540
GAACCCCCTA	GGGGGANTNA	TNCAAANCCC	CAGGATTGTC	CNCNCANGAA	ATCCCNANC	600
CCCNCCCTAC	CCNNCTTGG	GACNGTGACC	AANTCCCGGA	GTNCCAGTCC	GGCCNGNCTC	660
CCCCACCGGT	NNCCNTGGGG	GGGTGAANCT	CNGNNTCANC	CNGNCGAGGN	NTCGNAAGGA	720
ACCGGNCCTN	GGNCGAANNG	ANCNNTCNGA	AGNGCCNCNT	CGTATAACCC	CCCCTCNCCA	780
NCCNACNGNT	AGNTCCCCCC	CNGGGTNCGG	AANGG			815

(2) INFORMATION FOR SEQ ID NO:25:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 775 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCGAGATGTC	TCGCTCCGTG	GCCTTAGCTG	TGCTCGCGCT	ACTCTCTCTT	TCTGGCCTGG	60
AGGCTATCCA	CGTACTCCA	AAGATTCAAG	TTTACTCAGC	TCATCCAGCA	GAGAATGGAA	120
AGTCAAATTT	CCTGAATTGC	TATGTGTCG	GGTTTCATCC	ATCCGACATT	GAANTTGACT	180
TACTGAAGAA	TGGANAGAGA	ATTGAAAAAG	TGGAGCATTG	AGACTTGTCT	TTCAGCAAGG	240
ACTGGTCTTT	CTATCTCNTG	TACTACACTG	AATTCAACCC	CACTGAAAAAA	GATGAGTATG	300
CCTGGCGTGT	GAACCATGTG	ACTTTGTAC	AGCCCAAGAT	AGTTAACGTGG	GATCGAGACA	360
TGTAAGCAGN	CNNCATGGAA	GTGGAAGAT	GCCGCATTG	GATTGGATGA	ATTCCAAATT	420
CTGCTTGCTT	GCNTTTAAAT	ANTGATATGC	NTATACACCC	TACCTTTAT	GNCCCCAAAT	480
TGTAGGGTT	ACATNANTGT	TCNCNTNGGA	CATGATCTTC	CTTTATAANT	CCNCCNTTCG	540
AATTGCCCGT	CNCCCCNGTTN	NGAATGTTTC	CNNAACCACG	GTGGCTCCC	CCAGGTNC	600
TCTTACGGAA	GGGCCTGGGC	CNCTTNCAA	GGTTGGGGGA	ACCNAAAATT	TCNCTNTGC	660
CCNCCCNCCA	CNNTCTTNGN	NNCNCANTTT	GGAACCCCTTC	CNATTCCCCCT	TGGCCTCNNA	720
NCCTTNNCTA	ANAAAACTTN	AAACGTNGC	NAAANNTTTN	ACTTCCCCCC	TTACC	775

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 820 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

ANATTANTAC	AGTGTAACT	TTTCCCAGAG	GTGTGTANAG	GGAACGGGGC	CTAGAGGCAT	60
CCCANAGATA	NCTTATANCA	ACAGTGCTTT	GACCAAGAGC	TGCTGGGCAC	ATTCCTGCA	120
GAAAAGGTGG	CGGTCCCCAT	CACTCCTCCT	CTCCCATAGC	CATCCCAGAG	GGGTGAGTAG	180
CCATCANGCC	TTCGGTGGGA	GGGAGTCANG	GAAACAACAN	ACCACAGAGC	ANACAGACCA	240
NTGATGACCA	TGGGGGGGAG	CGAGCCTCTT	CCCTGNACCG	GGGTGGCANA	NGANAGCCTA	300
NCTGAGGGGT	CACACTATAA	ACGTTAACGA	CNAGATNAN	CACCTGCTTC	AAGTGCACCC	360
TTCCTACCTG	ACNACCAGNG	ACCNNAACT	GCNGCCTGGG	GACAGCNCTG	GGANCAGCTA	420
ACNAGCACT	CACCTGCC	CCCAGGCCG	TNCGCCTCCC	GGTCTGNC	AAGGGAAGCT	480
CCCTGTTGGA	ATTNCGGGG	NACCAAGGG	NCCCCCTCCT	CCANCTGTGA	AGGAAAANN	540
GATGGAATT	TNCCCTTCCG	GCCNNTCC	TCTTCTTTA	CACGCC	NNTACTCN	600

TCCCTCTNTT	NTCCTGNCNC	ACTTTTNACC	CCNNNATTTC	CCTTNATTGA	TCGGANNCTN	660
GANATTCCAC	TNNCGCTNC	CNTCNATCNG	NAANACNAAA	NACTNTCTNA	CCCNGGGAT	720
GGGNNCCTCG	NTCATCCTCT	CTTTTCNCT	ACCNCCNNTT	CTTGCCCTCT	CCTTNGATCA	780
TCCAACCNTC	GNTGGCCNTN	CCCCCCCNNN	TCCTTNCC			820

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 818 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

TCTGGGTGAT	GGCCTCTTCC	TCCTCAGGGA	CCTCTGACTG	CTCTGGGCCA	AAGAACATCT	60
TGTTTCTTCT	CCGAGCCCCA	GGCAGCGGTG	ATTCAAGCCCT	GCCCAACCTG	ATTCTGATGA	120
CTGCGGATGC	TGTGACGGAC	CCAAGGGCA	AATAGGGTCC	CAGGGTCCAG	GGAGGGGCGC	180
CTGCTGAGCA	CTTCCGCCCC	TCACCCCTGCC	CAGCCCCTGC	CATGAGCTCT	GGGCTGGTGC	240
TCCGCCTCCA	GGGTTCTGCT	CTTCCANGCA	NGCCANCAAG	TGGCGCTGGG	CCACACTGGC	300
TTCTTCTTGC	CCCNTCCCTG	GCTCTGANTC	TCTGTCTTCC	TGTCCTGTGC	ANGCNCCTTG	360
GATCTCAGTT	TCCCTCNCTC	ANNGAACTCT	GTTTCTGANN	TCTTCANTTA	ACTNTGANTT	420
TATNACCNAN	TGGNCTGTNC	TGTCNNACTT	TAATGGGCCN	GACCGGCTAA	TCCCTCCCTC	480
NCTCCCTTCC	ANNTCCNNNA	ACCNCGCTTC	CNTCCTCTCC	CCNTANCCCG	CCNGGGAAANC	540
CTCCTTTGCC	CTNACCAANG	GCCNNNACCG	CCCNTNNCTN	GGGGGGCNNG	GTNNCTNCNC	600
CTGNTNNCCC	CNCTCNCCNT	TNCCTCGTCC	CNNNNNGCNCN	NGNTNNNTNCN	NCNGTCCNN	660
TNNCTCTTCN	NGNTTCGNA	NGNTCNNTN	TNNNNNGNCN	NGNTNNNTNCN	TCCCTCTCNC	720
CNNNTGNANG	TNNNTNNNNC	NCNGNNCCCC	NNNNCNNNNN	NGGNNTNTNNN	TCTNCNCNGC	780
CCNNCCCCC	NGNATTAAGG	CCTCCNNCTC	CCGGCC			818

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 731 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

AGGAAGGGCG	GAGGGATATT	GTANGGGATT	GAGGGATAGG	AGNATAAANG	GGGAGGGTGT	60
TCCAACATG	ANGGTGNNGT	TCTCTTTGA	ANGAGGGTTG	NGTTTTTANN	CCNGGTGGGT	120
GATTNAACCC	CATTGTATGG	AGNAAAGGN	TTTNAGGGAT	TTTCGGCTC	TTATCAGTAT	180
NTANATTCT	GTNAATCGGA	AAATNATNTT	TCNNCNGAA	ATNTTGCTC	CCATCCGNAA	240
ATTNCTCCCG	GGTAGTGCAT	NTTNGGGGN	CNGCANGTT	TCCCAGGCTG	CTANAATCGT	300
ACTAAAGNTT	NAAGTGGGAN	TNCAAATGAA	AACCTNNCAC	AGAGNATCCN	TACCCGACTG	360
TNNNTTNCCT	TCGCCCTNTG	ACTCTGCNG	AGCCAATAC	CCNNNGNAT	GTCNCCNGN	420
NNNGCGNCNC	TGAAANNNC	TCGNNGCTNN	GANCATCANG	GGGTTTCGCA	TCAAAGCNCN	480
CGTTTCNCAT	NAAGGCACCT	TNGCCTCATC	CAACCNCTNG	CCCTCNNCCA	TTTNGCCGTC	540
NGGTTCNCT	ACGCTNNNTG	CNCCTNNNTN	GANATTTNC	CCGCCTNGGG	NAANCCTCCT	600
GNAATGGGTA	GGGNCTTNTC	TTTNACCNN	GNGGNTACT	AATCNCTNC	ACGCNTNCTT	660
TCTCNACCCC	CCCCCTTTT	CAATCCANC	GGCNAATGGG	GTCTCCCCNN	CGANGGGGG	720
NNNCCCANNC	C					731

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 822 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGGNCNC	TTCTATGANT	ANTNTTAGAT	60
CGCTCANACC	TCACANCCTC	CCNACNANGC	CTATAANGAA	NANNAATAGA	NCTGTNCNN	120
ATNTNTACNC	TCATANNCTC	CNNNACCCAC	TCCCTCTTAA	CCCNACTGT	GCCTATNGCN	180
TNNCTANTCT	NTGCCGCCTN	CNANCCACN	GTGGGCCNAC	CNCNNGNATT	CTCNATCTCC	240
TCNCCATNTN	GCCTANANTA	NGTNACATACC	CTATAACCTAC	NCCAATGCTA	NNNCTAACNC	300
TCCATNANTT	ANNNTAACTA	CCACTGACNT	NGACTTTCNC	ATNANCTCCT	AATTTGAATC	360
TACTCTGACT	CCCACNGCCT	ANNNATTAGC	ANCNTCCCCC	NACNATNTCT	CAACCAAATC	420
NTCAACAACC	TATCTANCTG	TCNCACCAACC	NTTNCCCTCG	ATCCCCNNAC	AACCCCCCTC	480
CCAAATACCC	NCCACCTGAC	NCCTAACCCN	CACCATCCCG	GCAAGCCNAN	GGNCATTAN	540
CCACTGGAAT	CACNATNGGA	AAAAAAAAC	CCNAACTCTC	TANCNENNAT	CTCCCCTAANA	600
AATNCTCCTN	NAATTACTN	NCANTNCCAT	CAANCCACN	TGAACNNAA	CCCCCTGTTT	660
TANATCCCTT	CTTTCGAAA	CCNACCCCTT	ANNNCCCAAC	CTTNGGGCC	CCCCNCTNC	720
CCNAATGAAG	GNCNCCCAAT	CNANGAAACG	NCCNTGAAAA	ANCNAGGCNA	ANANNNTCCG	780
CANATCCTAT	CCCTTANTTN	GGGGNCCCTT	NCCCNNGGCC	CC		822

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 787 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

CGGCCGCCTG	CTCTGGCACA	TGCCTCCTGA	ATGGCATCAA	AAGTGATGGA	CTGCCCATG	60
CTAGAGAAGA	CCTTCTCTCC	TACTGTCATT	ATGGAGCCCT	GCAGACTGAG	GGCTCCCC	120
GTCTGCAGGA	TTTGATGTCT	GAAGTCGTGG	AGTGTGGCTT	GGAGCTCTC	ATCTACATNA	180
GCTGGAAGCC	CTGGAGGGC	TCTCTGCCA	GCCTCCCC	TCTCTCCACG	CTCTCCANGG	240
ACACCAGGGG	CTCCAGGCAG	CCCATTATTC	CCAGNANGAC	ATGGTGTTC	TCCACGCGGA	300
CCCATGGGGC	CTGNAAGGCC	AGGGTCTCCT	TTGACACCAT	CTCTCCCGTC	CTGCCTGGCA	360
GGCCGTGGGA	TCCACTANTT	CTANAACGGN	CGCCACCNCG	GTGGGAGCTC	CAGCTTTG	420
TCCCNNTAAT	GAAGGTTAAT	TGCNCGCTTG	GCGTAAATCAT	NGGTCAAAC	TNTTCCCTGT	480
GTGAAATTGT	TTNTCCCTC	NCNATTCCNC	NCNACATACN	AACCCGGAAN	CATAAAGTGT	540
TAAAGCCTGG	GGGTNGCCTN	NNGAATNAAC	TNAACTCAAT	TAATTGGCTT	GGCTCATGGC	600
CCGCTTCCN	TTCNGGAAA	CTGTCNTCCC	CTGCTTNNNT	GAATCGGCCA	CCCCCNNGGG	660
AAAAGCGGTT	TGCNTTTNG	GGGGNTCCCT	CCNCTTCCCC	CCTCNCTAAN	CCCTNCGCCT	720
CGGTGTTNC	NGGTNGCGGG	GAANGGGNAT	NNNCTCCNC	NAAGGGGNG	AGNNNGNTAT	780
CCCCAAA						787

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:

 - (A) LENGTH: 799 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

TTTTTTTTTTT	TTTTTTGGC	GATGCTACTG	TTTAATTGCA	GGAGGTGGGG	GTGTGTGTAC	60
CATGTACAG	GGCTATTAGA	AGCAAGAAGG	AAGGAGGGAG	GGCAGAGCGC	CCTGCTGAGC	120
AACAAAGGAC	TCCTGCAGCC	TTCTCTGTCT	GTCTCTTGGC	GCAGGCACAT	GGGGAGGCCT	180
CCCGCAGGGT	GGGGGCCACC	AGTCAGGGG	TGGGAGCACT	ACANGGGTG	GGAGTGGTG	240
GTGGCTGGTN	CNAATGGCCT	GNACANATC	CCTACGATT	TTGACACCTG	GATTCACCA	300
GGGGACCTTC	TGTTCTCCA	NGNAACTTC	NTNNATCTCN	AAAGAACACA	ACTGTTCTT	360
CNGCANTTCT	GGCTGTTCAT	GGAAAGCACA	GGTGTCCNAT	TTNGGCTGGG	ACTTGGTACA	420
TATGGTTCCG	GCCCACCTCT	CCCNCTNAAN	AAGTAATTCA	CCCCCCCCCN	CCNTCTNTTG	480
CCTGGGCCCT	TAANTACCCA	CACCGGAACT	CANTTANTTA	TTCATCTTNG	GNTGGGCTTG	540
NTNATCNCCN	CCTGAANGCG	CCAAGTGAA	AGGCCACGCC	GTNCCCNCTC	CCCATAGNAN	600
NTTTTNNCNCNT	CANCTAATGC	CCCCCNNGC	ACNATCCAA	TCCCCCCCN	TGGGGCCCC	660
AGCCCANGGC	CCCCGNCTCG	GGNNNCNGN	CNCGNANTCC	CCAGGNTCTC	CCANTCNGNC	720
CCNNNGCNCC	CCCGCACGCA	GAACANAAGG	NTNGAGCCNC	CCGANNNNNN	NGGTNNNCAC	780
CTCGCCCCCCC	CCNNCGNNG					799

(2) INFORMATION FOR SEQ ID NO:32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 789 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

TTTTTTTTTTT	TTTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
TTTTNCCNAG	GGCAGGTTTA	TTGACAACCT	CNCGGACAC	AANCAGGCTG	GGGACAGGAC	120
GGCAACAGGC	TCCGGCGGCG	GC GGCGGCG	CCCTACCTGC	GGTACCAAAT	NTGCAGCCTC	180
CGCTCCCGCT	TGATNTTCT	CTGCAGCTGC	AGGAGTCCNT	AAAACAGGGC	CTCGGCCNTN	240
GGTGGGCACC	CTGGGATTN	AATTTCCACG	GGCACAATGC	GGTCGCANCC	CCTCACCAACC	300
NATTAGGAAT	AGTGGTNTTA	CCCNCNNCG	TTGGCNCACT	CCCCNTGGAA	ACCACTTNTC	360
GCGGCTCCGG	CATCTGGTCT	AAACCTTGC	AAACNCTGGG	GCCCTCTTTT	TGGTTANTNT	420
NCCNGCCACA	ATCATNACTC	AGACTGGNC	GGGCTGGCCC	AAAAAAANCN	CCCCAAACC	480
GGNCCATGTC	TTNNCGGGGT	TGCTGCNATN	TNCATCACCT	CCCGGGCNCA	NCAGGNCAAC	540
CCAAAAGTTC	TTGNGGCCN	CAAAAAANCT	CCGGGGGGNC	CCAGTTCAA	CAAAGTCATC	600
CCCTTGGCC	CCCAAATCCT	CCCCCGNNT	NCTGGGTTG	GGAAACCCACG	CCTCTNNCTT	660
TGGNNGCAA	GNTGGNTCCC	CCTTCGGGCC	CCCGTGGGCC	CCNNCTCTAA	NGAAAACNCC	720
NTCCTNNNCA	CCATCCCCC	NNGNNAAGNC	TANCAANGNA	TCCCTTTTT	TANAAACGGG	780
CCCCCCNCG						789

(2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 793 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

GACAGAACAT	GTTGGATGGT	GGAGCACCTT	TCTATACGAC	TTACAGGACA	GCAGATGGGG	60
AATTATGGC	TGTTGGAGCA	ATANAACCC	AGTCTACGA	GCTGCTGATC	AAAGGACTTG	120
GACTAAAGTC	TGATGAACCT	CCCAATCAGA	TGAGCATGGA	TGATTGGCCA	GAAATGAANA	180
AGAAAGTTC	AGATGTATTT	GCAAAGAAGA	CGAAGGCAGA	GTGGTGTCAA	ATCTTGACG	240
GCACAGATGC	CTGTGTGACT	CCGGTTCTGA	CTTTTGAGGA	GGTTGTTCAT	CATGATCACA	300

ACAANGAACG	GGGCTCGTT	ATCACCANTG	AGGAGCAGGA	CGTGAGCCCC	CGCCCTGCAC	360
CTCTGCTGTT	AAACACCCCCA	GCCATCCCTT	CTTCAAAAG	GGATCCACTA	CTTCTAGAGC	420
GGNCGCCACC	CGGGTGGAGC	TCCAGCTTT	GTTCCTTTA	GTGAGGGTTA	ATTGCGCGCT	480
TGGCGTAATC	ATGGTCATAN	CTGTTTCTG	TGTGAAATTG	TTATCCGCTC	ACAATTCCAC	540
ACAACATACG	ANCCGGAAGC	ATNAAATTAA	AAAGCCTGGN	GGTNGCCTAA	TGANTGAACT	600
NACTCACATT	AATTGGCTTT	GCGCTCACTG	CCCGCTTCC	AGTCGGAAA	ACCTGTCTT	660
GCCAGCTGCC	NTTAATGAAT	CNGGCCACCC	CCCGGGGAAA	AGGCNGTTG	CTTNTTGCGG	720
CGCNCTTCCC	GCTTCTCGC	TTCCGAANT	CCTTCCCCCC	GGTCTTCGG	CTTGCAGCNA	780
ACGGTATCNA	CCT					793

(2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 756 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

GCCGCGACCG	GCATGTACGA	GCAACTCAAG	GGCGAGTGG	ACCGTAAAAG	CCCCAATCTT	60
ANCAAGTGC	GGGAANAGCT	GGGTCGACTC	AAGCTAGTTC	TTCTGGAGCT	CAACTTCTTG	120
CCAACCACAG	GGACCAAGCT	GACCAAACAG	CAGCTAATT	TGGCCCGTGA	CATACTGGAG	180
ATCGGGGCC	AATGGAGCAT	CCTACGCAAN	GACATCCCCT	CCTTCGAGCG	CTACATGGCC	240
CAGCTCAAAT	GCTACTACTT	TGATTACAAN	GAGCAGCTCC	CCGAGTCAGC	CTATATGCAC	300
CAGCTTCTGG	GCCTCAACCT	CCTCTTCTG	CTGTCCTCAGA	ACCGGGTGGC	TGANTNCCAC	360
ACGGANTTGG	ANCCGCTGCC	TGCCCANA	CATACANACC	AATGCTACA	TCNACCAACCA	420
GTGTCCCTGGA	GCAATACTGA	TGGANGCG	CTACCNAAA	GTNTTCTGG	CCNAGGGTAA	480
CATCCCCCGC	CGAGAGCTAC	ACCTTCTTC	TTGACATCCT	GCTCGACACT	ATCAGGGATG	540
AAAATCGCNG	GGTTGCTCCA	GAAAGGCTNC	AANAANATCC	TTTCNCTGA	AGGCCCCCGG	600
ATNCNCTAGT	NCTAGAATCG	GCCCAGC	CGCGTGGANC	CTCCAACCTT	TCGTTNCCCT	660
TTACTGAGGG	TTNATTGCCG	CCCTTGGCGT	TATCATGGTC	ACNCCNGTTN	CCTGTGTTGA	720
AATTNTTAAC	CCCCCACAAT	TCCACGCCNA	CATTTG			756

(2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

GGGGATCTCT	ANATCNACCT	GNATGCATGG	TTGTCGGTGT	GGTCGCTGTC	GATGAANATG	60
AACAGGATCT	TGCCCTTGA	GCTCTCGGCT	GCTGNTTTA	AGTTGCTAG	TCTGCCGTCA	120
TAGTCAGACA	CNCTCTTGGG	CAAAAACAN	CAGGATNTGA	GTCTTGTATT	CACCTCCAAT	180
AATCTTCNGG	GCTGTCTGCT	CGGTGAAC	GATGACNANG	GGCAGCTGGT	TGTGTNTGAT	240
AAANTCCANC	ANGTTCTCC	TGGTGCAC	CCCTCAAAG	TTGTTCCGGC	CTTCATCAA	300
CTTCTNNAA	ANGANNANCC	CANCTTGTC	GAGCTGGNAT	TTGGANAACA	CGTCACTGTT	360
GGAAAATGAT	CCCAAATGGT	ATGTCATCCA	TCGCCTCTGC	TGCCTGCAA	AAACTTGCTT	420
GGCNAAATC	CGACTCCCCN	TCCTTGAAG	AAGCCNATCA	CACCCCCCTC	CCTGGACTCC	480
NNCAANGACT	CTNCCGCTNC	CCCNTCCNN	CAGGGTTGGT	GGCANNCCGG	GCCCNTGCGC	540
TTCTTCAGCC	AGTTCACNAT	NTTCATCAGC	CCCTCTGCCA	GCTGTTNTAT	TCCTTGGGG	600
GGAANCCGTC	TCTCCCTTCC	TGAANNAACT	TTGACCGTNG	GAATAGCCGC	GCNTCNCNT	660
ACNTNCTGGG	CGGGGTTCAA	ANTCCCTCCN	TTGNCCNTCN	CCTCGGGCCA	TTCTGGATTT	720
NCCNAACTTT	TTCCCTCCCC	CNCCCNCGG	NGTTTGCNTT	TTTCATNGGG	CCCCAACTCT	780

GCTNTTGGCC ANTCCCCTGG GGGCNTNTAN CNCCCCCTNT GGTCCCNTNG GGCC 834

(2) INFORMATION FOR SEQ ID NO:36:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 814 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

CGGNGCGCTTT	CCNGCCGCGC	CCCGTTCCA	TGACNAAGGC	TCCCTTCANG	TTAAATACNN	60
CCTAGNAAAC	ATTAATGGGT	TGCTCTACTA	ATACATCATA	CNAACCAGTA	AGCCCTGCCA	120
NAACGCCAAC	TCAGGCCATT	CCTACCAAAAG	GAAGAAAAGGC	TGGTCTCTCC	ACCCCCCTGTA	180
GGAAAGGCCT	GCCTTGTAAG	ACACCACAAAT	NCGGCTGAAT	CTNAAGTCTT	GTGTTTTACT	240
AATGGAAAAAA	AAAAATAAAC	AANAGGTTAAAT	GTTCTCATGG	CTGCCCACCG	CAGCCTGGCA	300
CTAAAACANC	CCAGCGCTCA	CTTCTGTTG	GANAAAATATT	CTTGCTCTT	TTGGACATCA	360
GGCTTGATGG	TATCACTGCCC	ACNTTCCAC	CCAGCTGGGC	NCCCTTCCCC	CATNTTTGTC	420
ANTGANCTGG	AAAGGCCTGAA	NCNTTACTCTC	CAAAGTCTC	NGCCCCACAAG	ACCGGCCACC	480
AGGGGANGTC	NTTNCAGTG	GATCTGCCAA	ANANTACCCN	TATCATCNNT	GAATAAAAAG	540
GCCCCCTGAAC	GANATGCTTC	CANCANCCCTT	TAAGACCCAT	AATCCTNGAA	CCATGGTGCC	600
CTTCCGGTCT	GATCCNAAAG	GAATGTTCTT	GGGTCCANT	CCCTCCTTTG	TTNCTTACGT	660
TGTNTTGGAC	CCNTGCTNGN	ATNACCCAAN	TGANATCCCC	NGAAGCACCC	TNCCCCCTGGC	720
ATTGANTTT	CNTAAATTCT	CTGCCCTACN	NCTGAAAGCA	CNATTCCCTN	GGCNCCNAAN	780
GGNGAACTCA	AGAAGGTCTN	NGAAAACCCA	CNCN			814

(2) INFORMATION FOR SEQ ID NO:37:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 760 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

GCATGCTGCT	CTTCCTCAA	GTTGTTCTT	TTGCCATAAC	AACCACCATA	GGTAAAGCGG	60
GCGCAGTGTT	CGCTGAAGGG	GTTGAGTAC	CAGCGCGGG	TGCTCTCC	GCAGAGTCCT	120
GTGTCTGGCA	GGTCCACGCA	ATGCCCTT	TCACTGGGG	AATGGATGCG	CTGGAGCTCG	180
TCNAANCCAC	TCTGTATTT	TTCACANGCA	GCCTCCTCCG	AAGCNTCCGG	GCAGTTGGGG	240
GTGTCGTCA	ACTCCACTAA	ACTGTGATN	CANCAGCCCA	TTGCTGCAGC	GGAACTGGGT	300
GGGTGACAG	GTGCCAGAAC	ACACTGGATN	GGCCTTCCA	TGGAAGGGCC	TGGGGAAAT	360
CNCCTNANCC	CAAACGTCTC	CTCAAAGGCC	ACCTTGACA	CCCCGACAGG	CTAGAAATGC	420
ACTCTTCTTC	CCAAAGGTAG	TTGTTCTTGT	TGCCAAGCA	NCCTCCANCA	AACCCAAANC	480
TTGAAAATC	TGCTCCGTGG	GGGTATNNN	TACCANGTT	GGGAAANAA	ACCCGGCNGN	540
GANCCNCCTT	GTGGAATGC	NAAGGNAATA	ATCCTCTGT	CTTGCTTGGG	TGGAANAGCA	600
CAATTGAAC	GTAAACNTTG	GGCCGNNTTC	CNCTNGGTG	GTCTGAAACT	AATCACCGTC	660
ACTGGAAAAAA	GGTANGTGCC	TTCCCTGAAT	TCCCAAANTT	CCCCCTNGNTT	TGGGTNNNTT	720
CTCCCTNCC	CTAAAATCG	TNTTCCCCCC	CCNTANGGCG			760

(2) INFORMATION FOR SEQ ID NO:38:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 724 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TTTTTTTTTT	TTTTTTTTTT	TTTTAAAAAA	CCCCCTCCAT	TGAATGAAAA	60	
CTTCCNAAAT	TGTCCAACCC	CCTCNNCCAA	ATNNCCATT	CGGGGGGGGG	GTTCCAAACC	120
CAAATTAAATT	TTGGANNTTA	AATTAAATNT	TNATTNGGGG	AANAANCCAA	ATGTNAAGAA	180
AATTAAACCC	ATTATNAACT	TAAATNCCTN	GAAACCCNTG	GNTTCCAAAAA	ATTTTAACC	240
CTTAAATCCC	TCCGAAATTG	NTAANGAAA	ACCAAATTCTN	CCTAAGGCTN	TTTGAAGGTT	300
NGATTTAAC	CCCCTTNANT	TNTTTTNACC	CNNNGCTNAA	NTATTTNGNT	TCCGGTGT	360
TCCTNTTAAN	CNTNGTAAC	TCCCGNTAAT	GAANNNCCT	AANCCAATT	AACCGAATT	420
TTTTGAATT	GGAAATTCCN	NGGAAATTNA	CCGGGTTTT	TCCCNTTTGG	GGGCCATNCC	480
CCCNCTTCG	GGGTTGGGN	NTAGGTGAA	TTTTNNNANG	NCCCAAAAAA	NCCCCAANA	540
AAAAAACTCC	CAAGNNTTAA	TTNGAATNTC	CCCCCTCCCA	GGCCTTTGG	GAAAGGNGGG	600
TTNTGGGGG	CCNGGGANTT	CNTTCCCCN	TTNCCNCCCC	CCCCCNGGT	AAANGTTAT	660
NGNNTTGGT	TTTGGGCC	CTTNANGGAC	CTTCGGATN	GAAATTAAAT	CCCCGGGNCG	720
GGCG						724

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

TTTTTTTTTT	TTTTCTTIG	CTCACATT	ATTTTATT	TGATTTTTTT	TAATGCTGCA	60
CAACACAATA	TTTATTTCAT	TTGTTCTT	TATTCATTT	TATTTGTTG	CTGCTGCTGT	120
TTTATTATT	TTTACTGAAA	GTGAGAGGGA	ACTTTGTGG	CCTTTTTCC	TTTTCTGTA	180
GGCCGCCTTA	AGCTTCTAA	ATTTGAAACA	TCTAAGCAAG	CTGAANGAA	AAGGGGGTT	240
CGCAAAATCA	CTCGGGGAA	NGGAAAGGTT	GCTTGTAA	TCATGCCCTA	TGGTGGGTGA	300
TTAACTGCTT	GTACAATTAC	NTTCAC	TAATTAATTG	TGCTNAANGC	TTAATTANA	360
CTTGGGGGTT	CCCTCCCCAN	ACCAACCCN	CTGACAAAAA	GTGCCNGCCC	TCAAATNATG	420
TCCCAGCCTT	CNTTGAAACA	CACNGCNGAA	NGTTCCTATT	NTCCCCNCNC	CAGGTNAAAA	480
TGAAGGGTTA	CCATNTTTAA	CNCCACCTCC	ACNTGGC	GCCTGAATCC	TCNAAAANCN	540
CCCTCAANCN	AATTNCTNNG	CCCCGGTCNC	GCNTNNGTCC	CNCCCGGGCT	CGGGGAANTN	600
CACCCCGNGA	ANNCNNNTNC	NAACNAAATT	CCGAAAATAT	TCCCNNTCNC	TCAATTCCCC	660
CNNAGACTNT	CCTCNCNAN	CNCAATTTC	TTTNNTCAC	GAACNCGNNC	CNNAAAATGN	720
NNNNCCNCTC	CNCTNGTCCN	NAATCNCAN	C			751

(2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

GTTGGTATT	CTGTAAGATC	AGGTGTCCT	CCCTCGTAGG	TTTAGAGGAA	ACACCCTCAT	60
AGATGAAAC	CCCCCGAGA	CAGCAGCACT	GCAACTGCCA	AGCAGCCGGG	GTAGGAGGGG	120
CGCCCTATGC	ACAGCTGGC	CCTTGAGACA	GCAGGGCTTC	GATGTCAGGC	TCGATGTCAA	180

TGGTCTGGAA	GCGGCGGCTG	TACCTGCGTA	GGGGCACACC	GTCAGGGCCC	ACCAGGAACT	240
TCTCAAAGTT	CCAGGCAACN	TCGTTGCGAC	ACACCGGAGA	CCAGGTGATN	AGCTTGGGT	300
CGGTCTATAAN	CGCGGTGGCG	TCGTGCGCTGG	GAGCTGGCAG	GGCTCCCCG	AGGAAGGCNA	360
ATAAAAGGTG	CGCCCCCGCA	CCGTTCANCT	CGCACCTCTC	NAANACCATG	ANGTTGGCT	420
CNAACCCACC	ACCANNCCGG	ACTTCCTTGA	NGGAATTCCC	AAATCTCTTC	GNTCTTGGC	480
TTCTNCTGAT	GCCCTANCTG	GTTGCCNGN	ATGCCAANCA	NCCCCAANCC	CGGGGTCC	540
AAANCACCCN	CCTCCTCNNT	TCATCTGGGT	TNTNTCCCC	GAACCNNTGGT	TCCTCTCAAG	600
GGANCCCAT	TCTCNACCAN	TACTCACCN	NCCCCCCNT	GNNACCCANC	CTTCTANNGN	660
TTCCCNCCTG	NCCTCTGGCC	CNTCAAANAN	GCTTNCACNA	CCTGGGTCTG	CCTTCCCCCC	720
TNCCTATCT	GNACCCNCN	TTTGTCTCAN	TNT			753

(2) INFORMATION FOR SEQ ID NO:41:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 341 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

ACTATATCCA	TCACAACAGA	CATGCTTCAT	CCCATAGACT	TCTTGACATA	GCTTCAAATG	60
AGTGAACCCA	TCCTTGATT	ATATACATAT	ATGTTCTCAG	TATTTGGGA	GCCTTTCCAC	120
TTCTTTAAC	CTTGTTCATT	ATGAACACTG	AAAATAGGAA	TTTGTGAAGA	GTTAAAAAGT	180
TATAGCTTGT	TTACGTAGTA	AGTTTTGAA	GTCTACATT	AATCCAGACA	CTTAGTTGAG	240
TGTTAAACTG	TGATTTTAA	AAAATATCAT	TTGAGAATAT	TCTTCAGAG	GTATTTCAT	300
TTTACTTTT	TGATTAATTG	TGTTTTATAT	ATTAGGGTAG	T		341

(2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

ACTTACTGAA	TTTAGTTCTG	TGCTCTCCT	TATTTAGTGT	TGTATCATAA	ATACTTTGAT	60
GTTCACAAACA	TTCTAAATAA	ATAATTTC	GTGGCTTCAT	A		101

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo spiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

ACATCTTTGT TACAGTCTAA GATGTGTTCT TAAATCACCA TTCCCTTCCTG GTCCTCACCC	60
TCCAGGGTGG TCTCACACTG TAATTAGAGC TATTGAGGAG TCTTTACAGC AAATTAAGAT	120
TCAGATGCCT TGCTAAGTCT AGAGTTCTAG AGTTATGTTT CAGAAAGTCT AAGAAACCCA	180
CCTCTTGAGA GGTCACTAA GAGGACTTAA TATTTCATAT CTACAAAATG ACCACAGGAT	240
TGGATACAGA ACGAGAGTTA TCCTGGATAA CTCAGAGCTG AGTACCTGCC CGGGGGCCGC	300
TCGAA	305

(2) INFORMATION FOR SEQ ID NO:44:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 852 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ACATAAATAT CAGAGAAAAG TAGTCTTTGA AATATTTACG TCCAGGAGTT CTTTGTTCCT	60
GATTATTTGG TGTGTGTTT GGTTTGTGTC CAAAGTATTG GCAGCTTCAG TTTTCATTT	120
CTCTCCATCC TCGGGCATTTC TTCCCAAATT TATATACAG TCTTCGTCCA TCCACACGCT	180
CCAGAATTTC TCTTTTGAG TAATATCTCA TAGTCGCGT GAGCTTTCA TAGGTCATGC	240
TGCTGTTGTT CTTCTTTTCA CCCCATAGCT GAGGCACTGC CTCTGATTTCA AAGAACCTGA	300
AGACCCCCCTC AGATCGGTCT TCCCATTAA TTAATCCTGG GTTCTTGTCT GGGTTCAAGA	360
GGATGTCGCG GATGAATTCC CATAAGTGG TCCCTCTCGG GTTGTGCTTT TTGGTGTGGC	420
ACTTGGCAGG GGGGTCTTGC CCCTTTTCA TATCAGGTGA CTCTGCAACA GGAAGGTGAC	480
TGGTGGTTGT CATGGAGATC TGAGCCGGC AGAAAGTTTT GCTGTCCAAC AAATCTACTG	540
TGCTACCATA GTTGGTGTCA TATAAAATAGT TCTNGTCTTT CAAGGTGTTC ATGATGAAAG	600
GCTCAGTTG TTCAGTCTTG ACAATGACAT TGTTGTGGA CTGGAACAGG TCACTACTGC	660
ACTGGCCGTT CCACTTCAGA TGCTGCAAGT TGCTGTAGAG GAGNTGCCCG GCCGTCCCTG	720
CCGCCCGGGT GAACTCCTGC AAACTCATGC TGCAAAGGTG CTCGCCGTG ATGTCGAAC	780
CNTGGAAAGG GATACAATTG GCATCCAGCT GTTGGTGTCA CAGGAGGTGA TGGAGCCACT	840
CCACACACTG GT	852

(2) INFORMATION FOR SEQ ID NO:45:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 234 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

ACAAACAGACC CTTGCTCGCT AACGACCTCA TGCTCATCAA GTTGGACGAA TCCGTGTCG	60
AGTCTGACAC CATCCGGAGC ATCAGCATTG CTTCGCAGTG CCCTACCGCG GGGAACTTT	120
GCCTCGTTTC TGGCTGGGGT CTGCTGGCGA ACGGCAGAAT GCCTACCGTG CTGCGATGCG	180

TGAACGTGTC GGTGGGTGCT GAGGGAGGTCT GCAGTAAGCT CTATGACCCG CTGT

234

(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 590 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

ACTTTTTATT TAAATGTTTA TAAGGCAGAT CTATGAGAAT GATAGAAAAAC ATGGTGTGTA	60
ATTGATAGC AATATTTGG AGATTACAGA GTTTAGTAA TTACCAATTAA CACAGTTAAA	120
AAGAAGATAA TATATTCCAA GCANATACAA AATATCTAAT GAAAGATCAA GGCAGGAAA	180
TGANTATAAC TAATTGACAA TGAAAATCA ATTAAATGT GAATTGCACA TTATCCTTTA	240
AAAGCTTTCA AAANAAANAA TTATTGCACT CTANTTAATT CAAACAGTGT TAAATGGTAT	300
CAGGATAAAAN AACTGAAGGG CANAAAGAAT TAATTTCAC TTCATGTAAC NCACCCANAT	360
TTACAATGGC TTAAATGCAN GGAAAAAGCA GTGGAAGTAG GGAAGTANTC AAGGTCTTC	420
TGGCTCTAA TCTGCCTAC TCTTTGGGTG TGGCTTGAT CCTCTGGAGA CAGCTGCCAG	480
GGCTCCTGTT ATATCCACAA TCCCAGCAGC AAGATGAAGG GATGAAAAAG GACACATGCT	540
GCCTTCCTTT GAGGAGACTT CATCTCACTG GCCAACACTC AGTCACATGT	590

(2) INFORMATION FOR SEQ ID NO:47:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 774 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

ACAAGGGGGC ATAATGAAGG AGTGGGGANA GATTTAAAG AAGGAAAAAA AACGAGGCC	60
TGAAACAGAAAT TTCTCTGNAC AACGGGGCTT CAAAATAATT TTCTTGGGG A GTTCAAGAC	120
GCTCACTGC TTGAAACTTAA AATGGATGTG GGACANAAATT TTCTGTAATG ACCCTGAGGG	180
CATTACAGAC GGGACTCTGG GAGGAAGGAT AAACAGAAAG GGGACAAAGG CTAATCCAA	240
AAACATCAAAG AAAGGAAGGT GGCGTCATAC CTCCCAGCCT ACACAGTTCT CCAGGGCTCT	300
CCTCATCCCT GGAGGACGAC AGTGGAGGAA CAACTGACCA TGTCCCCAGG CTCCCTGTG	360
CTGGCTCCTG GTCTTCAGCC CCCAGCTCTG GAAGCCCACC CTCTGCTGAT CCTGCGTGGC	420
CCACACTCCT TGAACACACA TCCCCAGGTT ATATCCTGG ACATGGCTGA ACCTCCTATT	480
CCTACTTCCG AGATGCCCTG CTCCCTGCAG CCTGTCAAAA TCCCACTCAC CCTCCAAACC	540
ACGGCATGGG AAGCCTTCT GACTTGCTCT ATTACTCCAG CATCTTGGAA CAATCCCTGA	600
TTCCCCACTC CTTAGAGGCA AGATAGGGTG GTTAAGAGTA GGGCTGGACC ACTTGGAGCC	660
AGGCTGCTGG CTTCAAATTN TGGCTCATT ACAGAGCTATG GGACCTTGGG CAAGTNATCT	720
TCACTTCTAT GGGCNCATT TGTTCTACC TGCAAAATGG GGGATAATAA TAGT	774

(2) INFORMATION FOR SEQ ID NO:48:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 124 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

CANAAATTGA AATTTATAA AAAGGCATTT TTCTCTTATA TCCATAAAAT GATATAATT	60
TTGCAANTAT ANAAATGTGT CATAAATTAT AATGTTCCCTT AATTACAGCT CAACGCAACT	120
TGGT	124

(2) INFORMATION FOR SEQ ID NO:49:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GCCGATGCTA CTATTTATT GCAGGAGGTG GGGGTGTTT TATTATTCTC TCAACAGCTT	60
TGTGGCTACA GGTGGTGTCT GACTGCATNA AAAANTTTT TACGGGTGAT TGCAAAAATT	120
TTAGGGCACC CATATCCCAA GCANTGT	147

(2) INFORMATION FOR SEQ ID NO:50:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 107 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

ACATTAAATT AATAAAAGGA CTGTTGGGT TCTGCTAAAA CACATGGCTT GATATATTGC	60
ATGGTTGAG GTTAGGAGGA GTTAGGCATA TGTTTGGGA GAGGGGT	107

(2) INFORMATION FOR SEQ ID NO:51:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 204 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GTCCCTAGGAA GTCTAGGGGA CACACGACTC TGGGGTCACG GGGCCGACAC ACTTGCACGG	60
CGGGAAGGAA AGGCAGAGAAA GTGACACCGT CAGGGGGAAA TGACAGAAAG GAAAATCAAG	120
GCCTTGCAAG GTCAGAAAGG GGACTCAGGG CTTCCACCAC AGCCCTGCC CACTTGGCCA	180
CCTCCCTTT GGGACCAAGCA ATGTT	204

(2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

ACAAAGATAAA CATTATCTT ATAACAAAAA TTTGATAGTT TTAAAGGTTA GTATTGTGTA	60
GGGTATTTTC CAAAAGACTA AAGAGATAAC TCAGGTTAAA AGTTAGAAAT GTATAAAACA	120
CCATCAGACA GGTTTTTAAA AAACAACATA TTACAAAATT AGACAATCAT CCTTAAAAAA	180
AAAACCTTCTT GTATCAATT CTGGTTCA AAATGACTGA CTTAANTATT TTTAAATATT	240
TCANAAACAC TTCCCTAAAG ATTTCANA TGGTAGCTTT CANATGTNCC CTCAGTCCC	300
ATGTTGCTCA GATAAAATAAA TCTCGTGAGA ACTTACCAACC CACCACAAGC TTTCTGGGC	360
ATGCAACAGT GTCTTTCTT TNCTTTTCTT TTTTTTTTT TTACAGGCAC AGAAACTCAT	420
CAATTATTATT TGGATAACAA AGGGTCTCCA AATTATATTG AAAAATAAAT CCAAGTTAAT	480
ATCACTCTTG T	491

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 484 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

ACATAATTAA GCAGGGCTAA TTACCATAAAG ATGCTATTAA TTAANAGGTN TATGATCTGA	60
GTATTAACAG TTGCTGAAGT TTGGTATTTT TATGCGACAT TTTCTTTTG CTTTGATAAC	120
ACTACAGAAC CCTTAAGGAC ACTGAAAATT AGTAAGTAA GTTCAGAAAC ATTAGCTGCT	180
CAATCAAATC TCTACATAAC ACTATAGTAA TTAAAACGTT AAAAAAAAGT GTTGAATCT	240
GCACTAGTAT ANACCGCTCC TGTCAGGATA ANACTGCTTT GGAACAGAAA GGGAAAANC	300
AGCTTTGANT TTCTTTGTGC TGATANGAGG AAAGGCTGAA TTACCTTGTT GCCTCTCCCT	360
AATGATTGGC AGGTCNGGTA AATNCCAAA CATATTCCAA CTCAACACTT CTTTCCNCG	420
TANCTTGANT CTGTGTATTTC CAGGANCAGG CGGATGGAAT GGGCCAGCCC NC GGATGTTCA CANT	480
	484

(2) INFORMATION FOR SEQ ID NO:54:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 151 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

ACTAACACCTC GTGCTTGTA ACTCCATACA GAAAACGGTG CCATCCCTGA ACACGGCTGG	60
CCACTGGGTA TACTGCTGAC AACCGCAACA ACAAAAACAC AAATCCTGG CACTGGCTAG	120
TCTATGTCCT CTCAAGTGCC TTTTTGTTG T	151

(2) INFORMATION FOR SEQ ID NO:55:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 91 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

ACCTGGCTTG TCTCCGGGTG GTTCCCCGGCG CCCCCCACGG TCCCCAGAAC GGACACTTTC	60
GCCCTCCAGT GGATACTCGA GCCAAAGTGG T	91

(2) INFORMATION FOR SEQ ID NO:56:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 133 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

GGCGGATGTG CGTTGGTTAT ATACAAATAT GTCATTTAT GTAAGGGACT TGAGTATACT	60
TGGATTTTG GTATCTGTGG GTTGGGGGA CGGTCCAGGA ACCAATACCC CATGGATAACC	120
AAGGGACAAAC TGT	133

(2) INFORMATION FOR SEQ ID NO:57:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 147 base pairs
 - (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

ACTCTGGAGA ACCTGAGCCG CTGCTCCGCC TCTGGGATGA GGTGATGCAN GCNGTGGCGC	60
GACTGGGAGC TGAGCCCTTC CCTTTGCGCC TGCCTCAGAG GATTGTTGCC GACNTGCANA	120
TCTCANTGGG CTGGATNCAT GCAGGGT	147

(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 198 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

ACAGGGATAT AGGTTTNAAG TTATTGTNAT TGAAAATAC ATTGAATTTT CTGTATACTC	60
TGATTACATA CATTATCCT TTAAAAAAGA TGAAATCTT AATTTTTATG CCATCTATTA	120
ATTACCAAT GAGTTACCTT GTAAATGAGA AGTCATGATA GCACTGAATT TAACTAGTT	180
TTGACTTCTA AGTTTGGT	198

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 330 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

ACAACAAATG GGTTGTGAGG AAGTCTTATC AGCAAAACTG GTGATGGCTA CTGAAAAGAT	60
CCATTGAAAA TTATCATTAA TGATTTAAA TGACAAAGTTA TCAAAAACTC ACTCAATTTC	120
CACCTGTGCT AGCTTGCTAA AATGGGAGTT AACTCTAGAG CAAATATAGT ATCTTCTGAA	180
TACAGTCAAT AAATGACAAA GCCAGGGCCT ACAGGTGGTT TCCAGACTTT CCAGACCCAG	240
CAGAAGGAAT CTATTTTATC ACATGGATCT CCGTCTGTGC TCAAAATACC TAATGATATT	300
TTTCGTCTTT ATTGGACTTC TTTGAAGAGT	330

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

ACCGTGGGTG CCTTCTACAT TCCTGACGGC TCCTTCACCA ACATCTGGTT CTACTTCGGC	60
GTCGTGGCT CCTTCCTCTT CATCCTCATC CAGCTGGTGC TGCTCATCGA CTTTGCGCAC	120
TCCCTGGAACC AGCGGTGGCT GGGCAAGGCC GAGGAGTGCG ATTCCCGTGC CTGGT	175

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 154 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

ACCCCACTTT TCCTCCTGTG AGCAGTCTGG ACTTCTCACT GCTACATGAT GAGGGTGAGT	60
GGTTGTTGCT CTTCAACAGT ATCCTCCCCT TTCCGGATCT GCTGAGCCGG ACAGCAGTGC	120
TGGACTGCAC AGCCCCGGGG CTCCACATTG CTGT	154

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 30 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

CGCTCGAGCC CTATAGTGAG TCGTATTAGA	30
----------------------------------	----

(2) INFORMATION FOR SEQ ID NO:63:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 89 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

ACAAAGTCATT TCAGCACCC TTGCTCTCA AACTGACCA TCTTTATAT TTAATGCTTC	60
CTGTATGAAT AAAATGGTT ATGTCAAGT	89

(2) INFORMATION FOR SEQ ID NO:64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

ACCGGAGTAA CTGAGTCGGG ACGCTGAATC TGAATCCACC AATAAAATAAA GGTTCTGCAG	60
AATCAGTGCA TCCAGGATTG GTCCTTGGAT CTGGGGT	97

(2) INFORMATION FOR SEQ ID NO:65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 377 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

ACAACAANAA NTCCCTTCTT TAGGCCACTG ATGGAAACCT GGAACCCCCCT TTTGATGGCA	60
GCATGGCGTC CTAGGCCTTG ACACAGCCGC TGGGGTTTGG GCTNTCCCAA ACCGCACACC	120
CCAACCCCTGG TCTACCCACA NTTCTGGCTA TGGGCTGTCT CTGCCACTGA ACATCAGGGT	180
TCGGTCATAA NATGAAATCC CAANGGGAC AGAGGTCAGT AGAGGAAGCT CAATGAGAAA	240
GGTGCTGTTT GTCAGCCAG AAAACAGCTG CCTGGCATTC GCCGCTGAAC TATGAACCCG	300
TGGGGGTGAA CTACCCCCAN GAGGAATCAT GCCTGGGCGA TGCAANGGTG CCAACAGGAG	360
GGGGGGGAGG AGCATGT	377

(2) INFORMATION FOR SEQ ID NO:66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 305 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

ACGCCTTTCC	CTCAGAATTTC	AGGGAAAGAGA	CTGTCGCCCTG	CCTTCCTCCG	TTGTTGGCTG	60
AGAACCGTG	TGCCCCTTCC	CACCATATCC	ACCCTCGCTC	CATCTTGAA	CTCAAACACG	120
AGGAACTAAC	TGCACCCCTGG	TCCTCTCCCC	AGTCCCCAGT	TCACCCCTCCA	TCCCCTCACCT	180
TCCTCCACTC	TAAGGGATAT	CAACACTGCC	CAGCACAGGG	GCCCCTGAATT	TATGTGGTTT	240
TTATATATTT	TTTAATAAGA	TGCACTTAT	GTCATTTTTT	AATAAAGTCT	GAAGAATTAC	300
TGTTT						305

(2) INFORMATION FOR SEQ ID NO:67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

ACTACACACA	CTCCACTTGC	CCTTGTGAGA	CACTTTGTCC	CAGCACTTTA	GGAATGCTGA	60
GGTCGGACCA	GCCACATCTC	ATGTGCAAGA	TTGCCAGCA	GACATCAGGT	CTGAGAGTTC	120
CCCTTTAAA	AAAGGGGACT	TGCTTAAAAAA	AGAAGTCTAG	CCACGATTGT	GTAGAGCAGC	180
TGTGCTGTGC	TGGAGATTCA	CTTTTGAGAG	AGTTCTCCTC	TGAGACCTGA	TCTTTAGAGG	240
CTGGGCAGTC	TTGCACATGA	GATGGGGCTG	GTCCTGATCTC	AGCACTCCTT	AGTCTGCTTG	300
CCTCTCCAG	GGCCCCAGCC	TGGCCACACC	TGCTTACAGG	GCACTCTCAG	ATGCCCATAC	360
CATAGTTCT	GTGCTAGTGG	ACCGT				385

(2) INFORMATION FOR SEQ ID NO:68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

ACTTAACCAG	ATATATTTTT	ACCCCAGATG	GGGATATTCT	TTGTAAAAAA	TGAAAATAAA	60
GTTTTTTAA	TGG					73

(2) INFORMATION FOR SEQ ID NO:69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 536 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGGGCTC TCACCCCTCCT	CTCCTGCAGC 60
TCCAGCTTTG TGCTCTGCCT CTGAGGAGAC CATGCCAG CATCTGAGTA CCCTGCTGCT	120
CCTGCTGGCC ACCCTAGCTG TGCCCCCTGGC CTGGAGCCCC AAGGAGGAGG ATAGGATAAT	180
CCCGGGTGGC ATCTATAACG CAGACCTCAA TGATGAGTGG GTACAGCGTG CCCTTCACCT	240
CGCCATCAGC GAGTATAACA AGGCCACCAA AGATGACTAC TACAGACGTC CGCTGCGGTT	300
ACTAAGAGCC AGGCAACAGA CCGTTGGGG GGTGAATTAC TTCTTCGACG TAGAGGTGGG	360
CCGAACCATA TGTACCAAGT CCCAGCCAA CTTGGACACC TGTGCCCTTC ATGAACAGCC	420
AGAACTGCAG AAGAACAGT TGTGCTCTT CGAGATCTAC GAAGTCCCT GGGGAGAACAA	480
GAANGTCCCT GGGTGAATC CAGGTGTCAA GAAATCCTAN GGATCTGTTG CCAGGC 536	

(2) INFORMATION FOR SEQ ID NO:70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 477 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

ATGACCCCTA ACAGGGGCCCT TCTCAGCCCT CCTAATGACC TCCGGCCTAG CCATGTGATT	60
TCACTTCCAC TCCATAACGC TCCTCATACT AGGCTACTA ACCAACACAC TAACCATATA	120
CCAATGATGG CGCGATGTAACACGAGAAG CACATACCAA GCCACCCACA CACCACCTGT	180
CCAAAAAGGC CTTCGATAGC GGATAATCCT ATTATTACCG TCAGAAGTTT TTTTCTTCGC	240
AGGGATTTTT CTGAGCCTTT TACCACTCCA GCCTAGCCCC TACCCCCAA CTAGGAGGGC	300
ACTGGCCCCC AACAGGCATC ACCCGCTAA ATCCCTAGA AGTCCCCTC CTAAACACAT	360
CCGTATTACT CGCATCAGGA GTATCAATCA CCTGAGCTCA CCATAGTCTA ATAGAAAACA	420
ACCGAAACCA AATTATTCAA AGCACTGCTT ATTACAATTT TACTGGGTCT CTATTTT 477	

(2) INFORMATION FOR SEQ ID NO:71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

AGAGCTATAG GTACAGTGTG ATCTCAGCTT TGCAACACAA TTTTCTACAT AGATAGTACT	60
AGGTATTAAT AGATATGTAAGAAGAAAT CACACCAATT ATAATGGTAA GATTGGTTTA	120
TGTGATTTA GTGGTATTT TGGCACCCCTT ATATATGTT TCCAAACTTT CAGCAGTGAT	180
ATTATTTCCTA TAACTTAAAAA AGTGAGTTG AAAAAGAAAAA TCTCCAGCAA GCATCTCATT	240
TAAATAAAGG TTTGTCTATCT TTAAAATAC AGCAATATGT GACTTTTAA AAAAGCTGTC	300
AAATAGGTGT GACCCTACTA ATAATTATTA GAAATACATT TAAAAACATC GAGTACCTCA	360
AGTCAGTTG CCTTGAAAAA TATCAAATAT AACTCTTAGA GAAATGTACA TAAAAGAATG	420
CTTCGTAATT TTGGAGTANG AGGTTCCCTC CTCAATTTG TATTTTAAA AAGTACATGG 480	

TAAAAAAA AATTACAAC AGTATATAAG GCTGTAAAT GAAGAATTCT GCC

533

(2) INFORMATION FOR SEQ ID NO:72:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 511 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

TATTACGGAA	AAACACACCA	CATAATTCAA	CTANCAAAGA	ANACTGCTTC	AGGGCGTGTAA	60
AAATGAAAGG	CTTCCAGGCA	GTTATCTGAT	AAAGAACAC	AAAAGAGGG	ACAAGGCTAA	120
AAGCCGCAGG	ATGTCTACAC	TATANCAGGC	GCTATTGGG	TTGGCTGGAG	GAGCTGTGGA	180
AAACATGGAN	AGATTGGTGC	TGGANATCGC	CGTGGCTATT	CCTCATTGTT	ATTACANAGT	240
GAGGTTCTCT	GTGTGCCAC	TGGTTGAAA	ACCGTTCTNC	ATAATGATA	GAATAGTACA	300
CACATGAGAA	CTGAAATGGC	CCAAACCCAG	AAAGAAAGCC	CAACTAGATC	CTCAGAANAC	360
GCTTCTAGGG	ACAATAACCG	ATGAAGAAAA	GATGGCCTCC	TTGTGCCCTT	GTCTGTTATG	420
ATTCTCTCC	ATTGCAGCNA	NAAACCCGT	CTTCTAAGCA	AACNCAGGTG	ATGATGGCNA	480
AAATACACCC	CCTCTTGAAG	NACCNGGAGG	A			511

(2) INFORMATION FOR SEQ ID NO:73:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 499 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

CAGTGCCAGC	ACTGGTGCCA	GTACCAAGTAC	CAATAACAGT	GCCAGTGCCA	GTGCCAGCAC	60
CAGTGGTGGC	TTCAGTGCTG	GTGCCAGCT	GACCGCCACT	CTCACATTG	GGCTCTTCGC	120
TGGCCTTGGT	GGAGCTGGTG	CCAGCACCAAG	TGGCAGCTCT	GGTGCCTGTG	GTTTCTCCTA	180
CAAGTGAGAT	TTTAGATATT	GTAACTCTG	CCAGTCCTTC	TCTTCAAGCC	AGGGTGCATC	240
CTCGAAACC	TACTCAACAC	AGCACTCTAG	GCAGCCACTA	TCAATCAATT	GAAGTTGACA	300
CTCTGCATTA	AATCTATTG	CCATTCTGA	AAAAAAAAAAA	AAAAAAAGGG	CGGCCGCTCG	360
ANTCTAGAGG	GCCCCTTAA	ACCCGCTGAT	CAGCCTCGAC	TGTGCCCTCT	ANTTGCCAGC	420
CATCTGTTGT	TTGCCCTTCC	CCCGNTGCCT	TCCTTGACCC	TGGAAAGTGC	CACTCCACT	480
GTCCTTTCCCT	AANTAAAAT					499

(2) INFORMATION FOR SEQ ID NO:74:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 537 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

TTTCATAGGA	GAACACACTG	AGGAGATACT	TGAAGAATT	GGATTCA	GCGAAGAGAT	60
TTATCAGCTT	AACTCAGATA	AAATCATTGA	AAAGTAATAAG	GTAAAAGCTA	GTCTCTA	120
TCCAGGCCCA	CGGCTCAAGT	GAATTGAA	ACTGCATT	CAGTAGAG	TAACACATAA	180
CATTGTATGC	ATGGAAACAT	GGAGGAACAG	TATTACAGTG	TCCTACC	CTAATCAAGA	240
AAAGAATTAC	AGACTCTGAT	TCTACAGTGA	TGATTGAATT	CTAAAAATGG	TAATCAT	300
GGCTTTGAT	TTATAANACT	TTGGGTACTT	ATACTAAATT	ATGGTAGTTA	TACTGCCTTC	360
CAGTTGCTT	GATATATTG	TTGATATTAA	GATTCTGAC	TTATATTTC	AATGGGTTCT	420
ACTGAAAAN	GAATGATATA	TTCTGAAGA	CATCGATATA	CATTTATT	CACTCTGAT	480
TCTACAATGT	AGAAAATGAA	GGAAATGCC	CAAATTGTAT	GGTGATAAAA	GTCCC	537

(2) INFORMATION FOR SEQ ID NO:75:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 467 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

CAAANACAAAT	TGTTCAAAAG	ATGCAAATGA	TACACTACTG	CTGCAGCTCA	CAAACACCTC	60
TGCATATTAC	ACGTACCTCC	TCCTGCTCT	CAAGTAGTGT	GGTCTATTTT	GCCATCATCA	120
CCTGCTGTCT	GCTTAGAAGA	ACGGCTTCT	GCTGCAANG	AGAGAAATCA	TAACAGACGG	180
TGGCACAAGG	AGGCCATCTT	TTCCCTCATCG	GTTATTGTCC	CTAGAAGCGT	CTTCTGAGGA	240
TCTAGTTGGG	CTTTCTTCT	GGGTTGGC	CATTTCANTT	CTCATGTGTG	TACTATTCTA	300
TCATTATTGT	ATAACGGTTT	TCAAACCN	GGGCACNCAG	AGAACCTCAC	TCTGTAATAA	360
CAATGAGGAA	TAGCCACGGT	GATCTCCAGC	ACCAAATCTC	TCCATGTTNT	TCCAGAGCTC	420
CTCCAGCCAA	CCCAAATAGC	CGCTGCTATN	GTGTAGAAC	TCCCTGN		467

(2) INFORMATION FOR SEQ ID NO:76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

AAGCTGACAG	CATTGGGCC	GAGATGTCTC	GCTCCGTGGC	CTTAGCTGTG	CTCGCGCTAC	60
TCTCTCTTTC	TGGCCTGGAG	GCTATCCAGC	GTACTCCAA	GATTCA	GTCAGGT	120
ATCCAGCAGA	GAATGGAAAG	TCAAATTCC	TGAATTGCTA	TGTGTCTGG	TTTCATCC	180
CCGACATTGA	AGTTGACTTA	CTGAAGAATG	GAGAGAGAAT	TGAAAAGTG	GAGCATT	240
ACTTGCTTT	CAGCAAGGAC	TGGTCTTCT	ATCTCTTGTA	CTACACTGAA	TTCACCCCA	300
CTGAAAAAGA	TGAGTATGCC	TGCCGTGTGA	ACCATGTGAC	TTTGTACAG	CCCAAGATNG	360

TTNAGTGGGA TCGANACATG TAAGCAGCAN CATGGGAGGT

400

(2) INFORMATION FOR SEQ ID NO:77:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

CTGGAGTGCC TTGGTGTTC AAGCCCCTC	AGGAAGCAGA ATGCACCTTC	TGAGGCACCT	60
CCAGCTGCC CGGGGGGG	TGCGAGGCTC GGAGCACCC	TGCCCGGCTG	120
CAGGCACTGT TCATCTCAGC	TTTCTGTCC CTTTGCTCCC	GGCAAGCGCT	180
GTCATATCT GGAGCCTGAT	GTCTTAACGA ATAAAGGTCC	CATGCTCCAC	240
AAAAAAAAAA		CCGAAAAAAA	248

(2) INFORMATION FOR SEQ ID NO:78:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 201 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

ACTAGTCCAG TGTGGTGGAA TTCCATTGTG TTGGGCCAA CACAATGGCT ACCTTTAAC	60
TCACCCAGAC CCCGCCCTGC CGGTGCCCA CGCTGCTGCT AACGACAGTA TGATGCTTAC	120
TCTGCTACTC GGAAACTATT TTTATGTAAT TAATGTATGC TTTCTTGTAA ATAAATGCCT	180
GATTTAAAAA AAAAAAAA A	201

(2) INFORMATION FOR SEQ ID NO:79:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 552 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

TCCCTTTGTT AGGTTTTGTA GACAACCTA GACCTAACT GTGTCACAGA CTTCTGAATG	60
TTTAGGCAGT GCTAGTAATT CCCTCGTAAT GATTCTGTTA TTACTTTCCCT ATTCTTATT	120
CCTCTTCTT CTGAAGATTAA ATGAAGTTGA AAATTGAGCT GGATAAAATAC AAAAGGTAG	180

TGTGATAGTA TAAGTATCTA AGTGCAGATG AAAGTGTGTT ATATATATCC ATTCAAAATT	240
ATGCAAGTTA GTAATTACTC AGGGTTAAC AAATTACTTT AATATGCTGT TGAACCTACT	300
CTGTTCTTG GCTAGAAAAA ATTATAAACA GGACTTTGTT AGTTGGGAA GCCAAATTGA	360
TAATATTCTA TGTTCTAAA GTTGGCTAT ACATAAANTA TNAAGAAATA TGGAATTAA	420
TTCCCAGGAA TATGGGGTTC ATTTATGAAT ANTACCCGGG ANAGAAGTTT TGANTNAAAC	480
CNGTTTGGT TAATACGTTA ATATGCTCN AATNAACAAG GCNTGACTTA TTTCCAAAAA	540
AAAAAAAAAA AA	552

(2) INFORMATION FOR SEQ ID NO:80:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 476 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

ACAGGGATTG GAGATGCTAA GGCCCCAGAG ATCGTTGAT CCAACCCTCT TATTTTCAGA	60
GGGGAAAATG GGGCTAGAA GTTACAGAGC ATCTAGCTGG TCGCTGGCA CCCCTGGCCT	120
CACACAGACT CCCGAGTAGC TGGGACTACA GGCACACAGT CACTGAAGCA GGCCCTGTTT	180
GCAATTCACTG TTGCCACCTC CAACTTAAC ATTCTTCATA TGTGATGTCC TTAGTCACTA	240
AGGTTAAACT TTCCCACCCA GAAAAGCAA CTTAGATAAA ATCTTAGAGT ACTTTCATAC	300
TCTCTAAGT CCTCTTCCAG CCTCACTTTG AGTCTCCCTT GGGGGTTGAT AGGAANTNTC	360
TCTTGGCTTT CTCAATAAAA TCTCTATCCA TCTCATGTTT AATTGGTAC GCNTAAAAAT	420
GCTGAAAAAA TTAAAATGTT CTGGTTTCNC TTTAAAAAAA AAAAAAAAAA AAAAAAA	476

(2) INFORMATION FOR SEQ ID NO:81:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

TTTTTTTTTG TATGCCNTCN CTGTGGNGTT ATTGTTGCTG CCACCCCTGGA GGAGCCCAGT	60
TTCTTCTGTA TCTTTCTTTT CTGGGGGATC TTCCTGGCTC TGCCCCCTCA TTCCCAGCCT	120
CTCATCCCCA TCTTGCACTT TTGCTAGGGT TGGAGGGCGCT TTCTGGTAG CCCCTCAGAG	180
ACTCAGTCAG CGGGATAAAG TCCTAGGGT GGGGGTGTG GCAAGCCGGC CT	232

(2) INFORMATION FOR SEQ ID NO:82:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 383 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

AGGCAGGGAGC AGAACGCTAAA GCCAAAGCCC AAGAACAGATG CGAGTGCCAG CACTGGTGCC	60
AGTACCACTGA CCAATAACAT GCCAGTGCCA GTGCCAGCAC CAGTGGTGGC TTCAGTGCTG	120
GTGCCAGCCT GACCGCCACT CTCACATTTG GGCTCTTCGC TGGCCTTGGT GGAGCTGGTG	180
CCAGCACCAG TGGCAGCTCT GGTGCTCTGTG GTTCTCCTA CAAGTGAGAT TTTAGATATT	240
GTAAATCCTG CCAGTCTTTC TCTTCAAGCC AGGGTGCATC CTCAGAAACC TACTCAACAC	300
AGCACTCTNG GCAGCCACTA TCAATCAATT GAAGTTGACA CTCTGCATTA AATCTATTTG	360
CCATTTCAAA AAAAAAAA AAA	383

(2) INFORMATION FOR SEQ ID NO:83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

ACCGAATTGG GACCGCTGGC TTATAAGCGA TCATGTCCTC CAGTATTACC TCAACGAGCA	60
GGGAGATCGA GTCTATAACGC TGAAGAAATT TGACCCGATG GGACAAACAGA CCTGCTCAGC	120
CCATCCTGCT CGGTTCTCCC CAGATGACAA ATACTCTCGA CACCGAATCA CCATCAAGAA	180
ACGCTTCAAG GTGCTCATGA CCCAGCAACC GCGCCCTGTC CTCTGAGGGT CCTTAAACTG	240
ATGTCTTTTC TGCCACCTGT TACCCCTCGG AGACTCCGTA ACCAAACTCT TC GGACTGTG	300
AGCCCTGATG CCTTTTTGCC AGCCATACTC TTTGGCCTCAGTCTCTCGT GGC GATTGAT	360
TATGCTTGTG TGAGGCAATC ATGGTGGCAT CACCCATNAA GGGAACACAT TTGANTTTT	420
TTTCNCATAT TTAAATTAC NACCAGAATA NTTCAGAATA AATGAATTGA AAAACTCTTA	480
AAAAAAA AAAA	494

(2) INFORMATION FOR SEQ ID NO:84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 380 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

GCTGGTAGCC TATGGCGTGG CCACGGANGG GCTCCTGAGG CACGGGACAG TGACTTCCA	60
AGTATCCTGC GCCGCGTCTT CTACCGTCCC TACCTGCAGA TCTTCGGCA GATTCCCCAG	120
GAGGACATGG ACGTGGCCCT CATGGAGCAC AGCAACTGCT CGTCGGAGCC CGGCTTCTGG	180
GCACACCCCTC CTGGGCCCA GGCAGGCACC TGCGTCTCCC AGTATGCCA CTGGCTGGTG	240
GTGCTGCTCC TCGTCATCTT CCTGCTCGTG GCCAACATCC TGCTGGTCAC TTGCTCATTG	300
CCATGTTCAAG TTACACATTC GGCAAAGTAC AGGGCAACAG CNATCTCTAC TGGGAAGGCC	360
AGCGTTNCCG CCTCATCCGG	380

(2) INFORMATION FOR SEQ ID NO:85:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 481 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

GAGTTAGCTC	CTCCACAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CCTCCCTGCAT	CTTGGGGCGG	CTAATATCCA	120
GGAAACTCTC	AATCAAGTCA	CCGTCNATNA	AACCTGTGGC	TGGTTCTGTC	TTCCGCTCGG	180
TGTGAAAGGA	TCTCCAGAAG	GAGTGCTCGA	TCTTCCCCAC	ACCTTTGATG	ACTTTATTGA	240
GTCGATTCTG	CATGTCCAGC	AGGAGGTTGT	ACCAGCTCTC	TGACAGTGAG	GTCACCAAGCC	300
CTATCATGCC	TTTGAACGTG	CCGAAGAACCA	CCGAGCCTTG	TGTGGGGGGGT	GNAGTCTCAC	360
CCAGATTCTG	CATTACCAGA	NAGCCGTGGC	AAAAGANATT	GACAACCTCGC	CCAGGNNGAA	420
AAAGAACACC	TCCTGGAAGT	GCTNGCCGCT	CCTCGTCCNT	TGGTGGNNNGC	GCNTNCCTT	480
T						481

(2) INFORMATION FOR SEQ ID NO:86:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 472 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGCTGCTG	AGAATTCA	60
ACTTGGAAAA	GCAACTTNA	GCCTGGACAC	TGGTATTAAA	ATTCAACAATA	TGCAACACTT	120
TAAACAGTGT	GTCAATCTGC	TCCCTTA	TGTCA	TACCA	AGTCTGGGAA	180
CCCTATTCA	ACCTGTTAAA	AGGGCGCTAA	GCATTTGA	TTCAACATCT	TTTTTTTTGA	240
CACAAGTCG	AAAAAAGCAA	AACTAAACAG	TTNTAATTT	GTAGCCAAT	TCACTTTCTT	300
CATGGGACAG	AGCCATTGAA	TTTAAAGC	AAATTGCATA	ATATTGAGCT	TTGGGAGCTG	360
ATATNTGAGC	GGAAGANTAG	CCTTTCTACT	TCACCAGACA	CAACTCCTT	CATATTGGGA	420
TGTTNACNAA	AGTTATGTCT	CTTACAGATG	GGATGCTTT	GTGCAATT	TG	472

(2) INFORMATION FOR SEQ ID NO:87:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 413 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

AGAAAACCAGT ATCTCTNAAA ACAACCTCTC ATACCTTGTG GACCTAATTT TGTGTGCGTG	60
TGTGTGTGCG CGCATATTAT ATAGACAGGC ACATTTTT TACTTTGTAAAGCTTATG	120
CCTCTTGGT ATCTATATCT GTGAAAGTTT TAATGATCTG CCATAATGTC TTGGGGACCT	180
TTGTCTTCTG TGTAATGGT ACTAGAGAAA ACACCTATNT TATGAGTCAA TCTAGTTNGT	240
TTTATTGAC ATGAAGGAAA TTCCAGATN ACAACACTNA CAAACTCTCC CTTGACTAGG	300
GGGGACAAAG AAAAGCANAA CTGAACATNA GAAACAATTN CCTGGTGAGA AATTNCATAA	360
ACAGAAATTG GGTNGTATAT TGAAANANNG CATCATTNAA ACGTTTTTTT TTT	413

(2) INFORMATION FOR SEQ ID NO:88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 448 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

CGCAGCGGGT CCTCTCTATC TAGCTCCAGC CTCTCGCCTG CCCCACCTCCC CGCGTCCCGC	60
GTCCTAGCCN ACCATGGCG GGCCCCCTGCG CGCCCCCGCTG CTCCCTGCTGG CCATCCTGGC	120
CGTGGCCCTG GCCGTGAGCC CGCGGCCGG CTCCAGTCCC GGCAAGCCCG CGCGCCTGGT	180
GGGAGGCCCA TGGACCCCCC GTGGAAGAAG AAGGTGTGCG GCGTGCCTG GACTTTGCCG	240
TCCGCNANTA CAACAAACCC GCAACNACTT TTACCNAGCN CGCGCTGCAG GTTGTGCCGC	300
CCCAANCAA TTGTACTNG GGGTAANTAA TTCTTGGAAAG TTGAACCTGG GCCAAACNNG	360
TTTACCAAGA CCNAGCCAATT TNGAACATT NCCCCTCCAT AACAGCCCT TTTAAAAAGG	420
GAANCANTCC TGNTCTTTCA CAAATTAA	448

(2) INFORMATION FOR SEQ ID NO:89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 463 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

GAATTTGTG CACTGGCCAC TGTGATGGAA CCATTGGGC AGGATGCTTT GAGTTTATCA	60
GTAGTGATTG TGCAAAGTT GGTGTTGAA CATGAGTATG TAAAATGTCA AAAAATTAGC	120
AGAGGTCTAG GTCTGCATAT CAGCAGACAG TTTGTCCGTG TATTTGTAG CCTTGAAGTT	180
CTCAGTGACA AGTTNNNTCT GATGCGAAGT TCTNATTCCA GTGTTTAGT CCTTGCATC	240
TTTNATGTTN AGACTTGCTT CTNTNAAATT GCTTTGTNT TCTGCAGGTA CTATCTGTGG	300
TTTAACAAA TAGAANNACT TCTCTGCTT GAANATTGAA ATATCTTACA TCTNAAAATN	360
AATTCTCTCC CCATANAAA ACCCANGCCC TTGGGANAAT TTGAAAANG GNTCCTTCNN	420
AATTCNNANA ANTCAGNTN TCATACAAACA NAACNGGANC CCC	463

(2) INFORMATION FOR SEQ ID NO:90:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 400 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

AGGGATTGAA	GGTCTNTNT	ACTGTCGGAC	TGTTCANCCA	CCAACTCTAC	AAGTTGCTGT	60
CTTCCACTCA	CTGCTGTAA	GCNTNTAAC	CCAGACTGTA	TCTTCATAAA	TAGAACAAAT	120
TCTTCACCAAG	TCACATCTTC	TAGGACCTTT	TTGGATTCAAG	TTAGTATAAG	CTCTTCCACT	180
TCCTTTGTTA	AGACTTCATC	TGGTAAAGTC	TTAAGTTTG	TAGAAAGGAA	TTTAATTGCT	240
CGTCTCTAA	CAATGTCCTC	TCCTTGAAGT	ATTTGGCTGA	ACAACCCACC	TNAAGTCCCT	300
TTGTGCATCC	ATTTAAATA	TACTTAATAG	GGCATTGGTN	CACTAGGTAA	AATTCTGCCA	360
GAGTCATCTG	TCTGCAAAAG	TTGCGTTAGT	ATATCTGCCA			400

(2) INFORMATION FOR SEQ ID NO:91:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 480 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:

GAGCTCGGAT	CCAATAATCT	TTGTCTGAGG	GCAGCACACA	TATNCAGTGC	CATGGNAACT	60
GGCTTACCCCC	ACATGGGAGC	AGCATGCCGT	AGNTATATAA	GGTCATTCCC	TGAGTCAGAC	120
ATGCCCTCTT	GACTACCGTG	TGCCAGTGCT	GGTGATTCTC	ACACACCTCC	NNCCGCTCTT	180
TGTGGAAAAAA	CTGGCACTTG	NCTGGAACTA	GCAAGACATC	ACTTACAAAT	TCACCCACGA	240
GACACTTGAA	AGGTGTAACA	AAGCGACTCT	TGCATTGCTT	TTTGTCCCTC	CGGCACCAGT	300
TGTCAAATACT	AACCCGCTGG	TTTGCCTCCA	TCACATTGT	GATCTGTAGC	TCTGGATACA	360
TCTCCTGACA	GTACTGAAGA	ACTTCTTCTT	TTGTTTCAA	AGCAACTCTT	GGTGCCTGTT	420
NGATCAGGTT	CCCATTTCCC	AGTCCGAATG	TTCACATGGC	ATATNTTACT	TCCCACAAAA	480

(2) INFORMATION FOR SEQ ID NO:92:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 477 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:

ATACAGCCCCA NATCCCACCA CGAACATGCG CTTGTTGACT GAGAACCTGA TGCAGGTCACT	60
GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGAAAG CGGTTGATGC TGCACTCCTT	120
CCCACGCAGG CAGCAGCGGG GCCGGTCAAT GAACTCCACT CGTGGCTTGG GGTTGACGGT	180
TAANTGCAGG AAGAGGCTGA CCACCTCGCG GTCCACCAGG ATGCCGACT GTGCAGGGACC	240
TGCAGCGAAA CTCCTCGATG GTCATGAGCG GGAAGCGAAT GANGCCCAGG GCCTTGCCCCA	300
GAACCTTCCG CCTGTTCTCT GGCGTCACCT GCAGCTGCTG CCGCTNACAC TCGGCCTCGG	360
ACCAAGGGAC AAACGGCGT GAACAGCCGC ACCTCACCGA TGCCCANTGT GTCGCGCTCC	420
AGGAACGGCN CCAGCGTGTG CAGGTCAATG TCGGTGAANC CTCCGCGGGT AATGGCG	477

(2) INFORMATION FOR SEQ ID NO:93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 377 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:

GAACGGCTGG ACCTTGCTC GCATTGTGCT GCTGGCAGGA ATACCTTGGC AAGCAGCTCC	60
AGTCGGAGCA GCCCCAGACC GCTGCCGCCC GAAGCTAACG CTGCCTCTGG CCTTCCCCCTC	120
CGCCCTCAATG CAGAACCCANT AGTGGGAGCA CTGTGTTTAG AGTTAAGAGT GAACACTGTN	180
TGATTTTACT TGGGAATTTC CTCTGTTATA TAGCTTTCC CAATGCTAAT TTCCAAACAA	240
CAACAACAAA ATAACATGTT TGCCTGTTNA GTTGTATAAA AGTANGTGAT TCTGTATNTA	300
AAGAAAATAT TACTGTTACA TATACTGCTT GCAANTCTG TATTTATTGG TNCTCTGGAA	360
ATAAAATATAT TATTTAAA	377

(2) INFORMATION FOR SEQ ID NO:94:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:

CCCTTTGAGG GGTTAGGGTC CAGTCCCAG TGGAAAGAAC AGGCCAGGAG AANTGCGTGC	60
CGAGCTGANG CAGATTTCCC ACAGTGACCC CAGAGCCCTG GGCTATAGTC TCTGACCCCT	120
CCAAGGAAAG ACCACCTTCT GGGGACATGG GCTGGAGGGC AGGACCTAGA GGCACCAAGG	180
GAAGGCCCA TTCCGGGGCT GTTCCCCGAG GAGGAAGGGA AGGGGCTCTG TGTCCCCCCC	240
ACGAGGAANA GGCCCTGANT CCTGGGATCA NACACCCCT CACGTGTATC CCCACACAAA	300
TGCAAGCTCA CCAAGGTCCC CTCTCAGTCC CTTCCCTACA CCCTGAACGG NCAC TGGCCC	360
ACACCCACCC AGANCANCCA CCCGCCATGG GGAATGTNCT CAAGGAATCG CNGGGCAACG	420
TGGACTCTNG TCCCNNAAGG GGGCAGAATC TCCAATAGAN GGANNGAAC CTTGCTNANA	480
AAAAAAAANA AAAAAA	495

(2) INFORMATION FOR SEQ ID NO:95:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 472 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATT	120
TAGCTGTTT	GAGTTGATT	GCACCACTGC	ACCACAACTC	AATATGAAAA	CTATTTNACT	180
TATTATTAT	CTTGTGAAA	GTATACAATG	AAAATTTGT	TCATACTGTA	TTTATCAAGT	240
ATGATGAAA	GCAATAGATA	TATATTCTTT	TATTATGTTN	AATTATGATT	GCCATTATTA	300
ATCGGCAAA	TGTGGAGTGT	ATGTTCTTT	CACAGTAATA	TATGCCCTTT	GTAACCTCAC	360
TTGGTTATT	TATTGTAAT	GAATTACAAA	ATTCTTAATT	TAAGAAAATG	GTANGTTATA	420
TTTANTTCAN	TAATTCTTT	CCTGTTTAC	GTAAATT	AAAAGAATGC	AT	472

(2) INFORMATION FOR SEQ ID NO:96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 476 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

CTGAAGCATT	TCTTCAAACT	TNTCTACTTT	TGTCATTGAT	ACCTGTAGTA	AGTTGACAAT	60
GTTGGTAAAT	TTCAAAATT	TATGTAAC	CTACTAGTT	TACTTTCTCC	CCCAAGTC	120
TTTTAACTCA	TGATTTTAC	ACACACAATC	CAGAACTTAT	TATATAGCCT	CTAAAGTC	180
ATTCTTCACA	GTAGATGATG	AAAGAGTC	CCAGTGTCTT	GNGCANAATG	TTCTAGNTAT	240
AGCTGGATAC	ATACNGTGGG	AGTTCTATAA	ACTCATACCT	CAGTGGGACT	NAACCAAAT	300
TGTGTTAGTC	TCAATTCTA	CCACACTGAG	GGAGCCTCCC	AAATCACTAT	ATTCTTATCT	360
GCAGGTACTC	CTCCAGAAA	ACNGACAGGG	CAGGCTTGCA	TGAAAAAGTN	ACATCTGCGT	420
TACAAAGTCT	ATCTTCCTCA	NANGTGTN	AAGGAACAAT	TTAATCTTCT	AGCTTT	476

(2) INFORMATION FOR SEQ ID NO:97:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

ACTCTTTCTA	ATGCTGATAT	GATCTTGAGT	ATAAGAATGC	ATATGTCACT	AGAATGGATA	60
------------	------------	------------	------------	------------	------------	----

AAATAATGCT GCAAACCTAA TGTTCTTATG CAAAATGGAA CGCTAATGAA ACACAGCTTA	120
CAATCGAAA TCAAAACTCA CAAGTGCTCA TCTGTTGTAG ATTTAGTGTAA ATAAGACTTA	180
GATTGTGCTC CTTCGGATAT GATTGTTCT CANATCTTGC GCAATNTTC TTAGTCAAAT	240
CAGGCTACTA GAATTCTGTT ATTGGATATN TGAGAGCATG AAATTTTAA NAATACACTT	300
GTGATTATNA AATTAATCAC AAATTCACT TATAACCTGCT ATCAGCAGCT AGAAAAACAT	360
NTNNNTTTTA NATCAAAGTA TTTTGTGTTT GGAANTGTNN AAATGAAATC TGAATGTGGG	420
TTCNATCTTA TTTTTCCCN GACNACTANT TNCTTTTTA GGGNCTATTG TGANCCATC	479

(2) INFORMATION FOR SEQ ID NO:98:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 461 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

AGTGACTTGT CCTCCAACAA AACCCCTTGA TCAAGTTGT GGCACGTGACA ATCAGACCTA	60
TGCTAGTTCC TGTCACTCTAT TCGCTACTAA ATGCAGACTG GAGGGGACCA AAAAGGGGCA	120
TCAACTCCAG CTGGATTATT TTGGAGCTG CAAATCTATT CCTACTTGTA CGGACTTTGA	180
AGTGATTCAAG TTTCTCTAC GGATGAGAGA CTGGCTCAAG AATATCCTCA TGCAGCTTTA	240
TGAAGCCACT CTGAACACGC TGGTTATCTA GATGAGAACAA GAGAAATAAA GTCAAGAAAAT	300
TTACCTGGAG AAAAGAGGCT TTGGCTGGGG ACCATCCCCT TGAACCTTCT CTTAAGGACT	360
TTAAGAAAAA CTACCACATG TTGTGTATCC TGGTGCCGGC CGTTTATGAA CTGACCACCC	420
TTTGGAAATAA TCTTGACGCT CCTGAACCTG CTCCCTGCG A	461

(2) INFORMATION FOR SEQ ID NO:99:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 171 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GTGGCCGCGC GCAGGTGTTT CCTCGTACCG CAGGGCCCCC TCCCTTCCCC AGGCCTCCCT	60
CGGGCGCTCT GCGGGCCCGA GGAGGAGCGG CTGGCGGGTG GGGGGAGTGT GACCCACCC	120
CGGTGAGAAA AGCCTTCTCT AGCGATCTGA GAGGCCTGCC TTGGGGTAC C	171

(2) INFORMATION FOR SEQ ID NO:100:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 269 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

CGGCCGCAAG	TGCAACTCCA	GCTGGGGCCG	TGCGGACGAA	GATTCTGCCA	GCAGTTGGTC	60
CGACTGCGAC	GACGGCGGG	GCGACAGTCG	CAGGTGCAGC	GCGGGCGCCT	GGGGTCTTGC	120
AAGGCTGAGC	TGACGCCGCA	GAGGTCTGT	CACCTCCCAC	GACCTTGACG	CCGTCGGGGA	180
CAGCCGGAAC	AGAGCCCGGT	GAAGCGGGAG	GCCTCGGGGA	GCCCCCTCGGG	AAGGGCGGCC	240
CGAGAGATAC	GCAGGTGCAG	GTGGCCGCC				269

(2) INFORMATION FOR SEQ ID NO:101:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 405 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:

TTTTTTTTTT	TTTTGGAATC	TACTGCGAGC	ACAGCAGGTC	AGCAACAAGT	TTATTTGCA	60
GCTAGCAAGG	TAACAGGGTA	GGGCATGGTT	ACATGTTAG	GTCAACTTCC	TTTGTCTGTGG	120
TTGATTGGTT	TGTCTTTATG	GGGGCGGGGT	GGGGTAGGGG	AAACGAAGCA	AATAACATGG	180
AGTGGGTGCA	CCCTCCCTGT	AGAACCTGGT	TACAAAGCTT	GGGGCAGTTC	ACCTGGTCTG	240
TGACCGTCAT	TTTCTTGACA	TCAATGTTAT	TAGAAGTCAG	GATATCTTTT	AGAGAGTCCA	300
CTGTTCTGGA	GGGAGATTAG	GGTTCTTGC	CAAATCCAAC	AAAATCCACT	GAAAAAGTTG	360
GATGATCAGT	ACGAATACCG	AGGCATATTTC	TCATATCGGT	GGCCA		405

(2) INFORMATION FOR SEQ ID NO:102:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 470 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:

TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	TTTTTTTTTT	60
GGCACTTAAT	CCATTTTAT	TTCAAAATGT	CTACAAATT	AATCCCATTA	TACGGTATTT	120
TCAAAATCTA	AATTATTCAA	ATTAGCCAA	TCCTTACCAA	ATAATACCA	AAAATCAAA	180
ATATACCTCT	TTCAGCAAAC	TTGTTACATA	AATTAAAAAA	ATATATACGG	CTGGTGTGTT	240
CAAAGTACAA	TTATCTTAAC	ACTGCAAACA	TTTAAGGAA	CTAAAATAAA	AAAAAACACT	300
CCGCAAAGGT	TAAAGGGAAC	ACAAATTCT	TTTACAACAC	CATTATAAAA	ATCATATCTC	360
AAATCTTAGG	GGAATATATA	CTTCACACGG	GATCTTAAC	TTTACTCACT	TTGTTTATTT	420
TTTTAAACCA	TTGTTTGGGC	CCAACACAAT	GGAAATCCCC	CTGGACTAGT		470

(2) INFORMATION FOR SEQ ID NO:103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 581 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:

TTTTTTTTTT TTTTTTTG	CCCCCTCTT	ATAAAAAAC	AGTTACCATT	TTATTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATCAAAA	GGCAGCTTTT	120
TAAATGGAAA	CTGCCTTAGA	TACATAATT	TTAGGAATT	GCTTAAAATC	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGTAAAAC	240
ATTTTCTTG	TCTTTAAAAT	TATCTAATCT	TTCCATT	TCCCTATTCC	300
GCTTCTCTAG	CCTCATTTTC	TAGCTCTTAT	CTACTATTAG	AAAGTCAATT	360
AGGGAAAACA	GGAAGAGAAA	TGGCACACAA	AACAAACATT	TTATATTCA	420
ACGTTAAATA	AATAGCATTT	TGTGAAGCCA	GCTCAAAAGA	AGGCTTAGAT	480
CCATTTTAGT	CACTAACACGA	TATCAAAGTG	CCAGAACATG	AAAGGTTTGT	540
TCAAAAGCTA	ATATAAGATA	TTTCACATAC	TCATCTTCT	G	581

(2) INFORMATION FOR SEQ ID NO:104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 578 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:

TTTTTTTTTT TTTTTCTCTT	CTTTTTTTTT GAAATGAGGA	TCGAGTTTT	60	
CACTCTCTAG	ATAGGGCATG	AAGAAAAC	TCATTTCCAG	120
CTCTTATGCT	ATATCATATT	TTAAGTAA	CTAATGAGTC	180
AGGAAATCTG	TTCATTCTTC	TCATTATAT	AGTTATATCA	240
GAGGTTTTTC	TCCTCTATT	ACACATAT	AGTACTACCT	300
TTCATGCAA	CTAGAAAATA	ATGTTCTT	TGCATAAGAG	360
CAAATTGCT	CAAATTGTT	GTAAAGTT	AAAGAGAACAA	420
AAATCACATT	TACGACAGCA	ATAATAAAC	TGAAGTACCA	480
AAAGGAACAT	TTTTAGCCTG	GGTATAATTA	GTAAATTATC	540
TGAATTACAC	TGTTATTATT	CCTAGCCCAA	TTTACAAGCA	578

(2) INFORMATION FOR SEQ ID NO:105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 538 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:

TTTTTTTTT	TTTTTCAGTA	ATAATCAGAA	CAATATTTAT	TTTTATATTAA	AAAATTCTATA	60
GAAAAGTGCC	TTACATTTAA	AAAAGTTG	TTTCTCAAAG	TGATCAGAGG	AATTAGATAT	120
GTCTTGAACA	CCAATATTTAA	TTTGAGGAAA	ATACACCAAA	ATACATTAAG	AAATTATTT	180
AAGATCATAG	AGCTTGTAAG	TGAAAAGATA	AAATTGACC	TCAGAAACTC	TGAGCATTAA	240
AAATCCACTA	TTAGCAAATA	AATTACTATG	GACTTCTTGC	TTAATTTG	TGATGAATAT	300
GGGGTGTAC	TGGTAAACCA	ACACATTCTG	AAGGATACAT	TACTTAGTGA	TAGATTCTTA	360
TGTACTTTGC	TAATACGTGG	ATATGAGTTG	ACAAGTTCT	CTTCTTCAA	TCTTTAAGG	420
GGCGAGAAAAT	GAGGAAGAAA	AGAAAAGGAT	TACCGATACT	GTTCTTCTA	TGGAAGGATT	480
AGATATGTTT	CCTTGCCAA	TATTAAGAAA	ATAATAATGT	TTACTACTAG	TGAAACCC	538

(2) INFORMATION FOR SEQ ID NO:106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 473 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:

TTTTTTTTT	TTTTTAGTC	AAGTTCTAT	TTTTATTATA	ATTAAGTCT	TGGTCATTTC	60
ATTATTAGC	TCTGCACTT	ACATATTAA	ATTAAGAAA	CGTTTAGAC	AACTGTACAA	120
TTATAAAATG	TAAGGTGCCA	TTATTGAGTA	ATATATTCT	CCAAGAGTGG	ATGTGTCCCT	180
TCTCCCACCA	ACTAATGAAC	AGAACACATTA	GTTAATTTC	ATTAGTAGAT	ATACACTGCT	240
GCAAACGCTA	ATTCTCTTCT	CCATCCCCAT	GTGATATTGT	GTATATGTGT	GAGTTGGTAG	300
AATGCATCAC	AATCTACAAT	CAACAGCAAG	ATGAAGCTAG	GCTGGGCTTT	CGGTGAAAAT	360
AGACTGTGTC	TGTCTGAATC	AAATGATCTG	ACCTATCCTC	GGTGGCAAGA	ACTCTTCGAA	420
CCGCTTCCTC	AAAGGCCTG	CCACATTGT	GGCTCTTGC	ACTTGTTC	AAA	473

(2) INFORMATION FOR SEQ ID NO:107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1621 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:

CGCCATGGCA	CTGCAGGGCA	TCTCGGTAT	GGAGCTGTCC	GGCCTGGCCC	CGGGCCCGTT	60
CTGTGCTATG	GTCTGGCTG	ACTTCGGGGC	GCCTGTGGTA	CGCGTGGACC	GGCCCGGCTC	120
CCGCTACGAC	GTGAGCCGCT	TGGGCCGGG	CAAGCGCTCG	CTAGTGCTGG	ACCTGAAGCA	180
GCCGCGGGGA	GCCGCCGTGC	TGCGCGTCT	GTGCAAGCGG	TGGATGTGC	TGCTGGAGCC	240
CTTCCGCCGC	GGTGTATGG	AGAAACTCCA	GCTGGGCCA	GAGATTCTGC	AGCGGGAAAAA	300
TCCAAGGCTT	ATTATGCCA	GGCTGAGTGG	ATTGGCCAG	TCAGGAAGCT	TCTGCCGTT	360
AGCTGGCCAC	GATATCAACT	ATTTGGCTT	GTCAGGTGTT	CTCTAAAAAA	TTGGCAGAAG	420
TGGTGAGAAT	CCGTATGCC	CGCTGAATCT	CCTGGCTGAC	TTTGCTGGTG	GTGGCTTAT	480
GTGTGCAC	GGCATTATAA	TGGCTTTT	TGACCGCACA	CCCACTGACA	AGGGTCAGGT	540

CATTGATGCA AATATGGTGG AAGGAACAGC ATATTTAAGT TCTTTCTGT GGAAAACCTCA 600
 GAAATCGAGT CTGTGGGAAG CACCTCGAGG ACAGAACATG TTGGATGGTG GAGCACCTT 660
 CTATACGACT TACAGGACAG CAGATGGGA ATTCAATGGCT GTTGGAGCAA TAGAACCCCA 720
 GTTCTACGAG CTGCTGATCA AAGGACTTGG ACTAAAGTCT GATGAACCTTC CCAATCAGAT 780
 GAGCATGGAT GATTGGCCAG AAATGAAGAA GAAGTTGCA GATGTATTTG CAAAGAAGAC 840
 GAAGGCAGAG TGGTGTCAAA TCTTTGACGG CACAGATGCC TGTGTGACTC CGGTTCTGAC 900
 TTTTGAGGAG GTTGTTCATC ATGATCACAA CAAGGAACGG GGCTCGTTA TCACCACTG 960
 GGAGCAGGAC GTGAGCCCCC GCCCTGCACC TCTGCTGTT AACACCCCG CCATCCCTTC 1020
 TTCAAAAGG GATCCTTTCA TAGGAGAAC CACTGAGGAG ATACTTGAAG AATTTGGATT 1080
 CAGCCGCAA GAGATTATC AGCTTAACCTC AGATAAAATC ATTGAAAGTA ATAAGGTAAA 1140
 AGCTAGTCTC TAACCTCCAG GCCCACGGCT CAAGTGAATT TGAATACTGC ATTTACAGTG 1200
 TAGAGTAACA CATAACATTG TATGCATGGA AACATGGAGG AACAGTATTAA CAGTGTCTA 1260
 CCACTCTAAAT CAAGAAAAGA ATTACAGACT CTGATTCTAC AGTGATGATT GAATTCTAAA 1320
 AATGGTTATC ATTAGGGCTT TTGATTTTATA AAACCTTGGG TACTTATACT AAATTATGGT 1380
 AGTATTCTG CCTTCCAGTT TGCTTGTAT ATTGTTGTAT ATTAAGATT TTGACTTATA 1440
 TTTGAAATGG GTTCTAGTGA AAAAGGAATG ATATATTCTT GAAGACATCG ATATACATT 1500
 ATTACACTC TTGATTCTAC AATGTAGAAA ATGAGGAAAT GCCACAAATT GTATGGTGAT 1560
 AAAAGTCACG TGAAACAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA 1620
 A 1621

(2) INFORMATION FOR SEQ ID NO:108:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 382 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:

Met	Ala	Leu	Gln	Gly	Ile	Ser	Val	Met	Glu	Leu	Ser	Gly	Leu	Ala	Pro
1		5						10					15		
Gly	Pro	Phe	Cys	Ala	Met	Val	Leu	Ala	Asp	Phe	Gly	Ala	Arg	Val	Val
					20				25				30		
Arg	Val	Asp	Arg	Pro	Gly	Ser	Arg	Tyr	Asp	Val	Ser	Arg	Leu	Gly	Arg
	35						40				45				
Gly	Lys	Arg	Ser	Leu	Val	Leu	Asp	Leu	Lys	Gln	Pro	Arg	Gly	Ala	Ala
	50					55			60						
Val	Leu	Arg	Arg	Leu	Cys	Lys	Arg	Ser	Asp	Val	Leu	Leu	Glu	Pro	Phe
	65				70				75				80		
Arg	Arg	Gly	Val	Met	Glu	Lys	Leu	Gln	Leu	Gly	Pro	Glu	Ile	Leu	Gln
	85					90				95					
Arg	Glu	Asn	Pro	Arg	Leu	Ile	Tyr	Ala	Arg	Leu	Ser	Gly	Phe	Gly	Gln
	100					105			110						
Ser	Gly	Ser	Phe	Cys	Arg	Leu	Ala	Gly	His	Asp	Ile	Asn	Tyr	Leu	Ala
	115					120			125						
Leu	Ser	Gly	Val	Leu	Ser	Lys	Ile	Gly	Arg	Ser	Gly	Glu	Asn	Pro	Tyr
	130					135			140						
Ala	Pro	Leu	Asn	Leu	Leu	Ala	Asp	Phe	Ala	Gly	Gly	Leu	Met	Cys	
	145					150			155			160			
Ala	Leu	Gly	Ile	Ile	Met	Ala	Leu	Phe	Asp	Arg	Thr	Arg	Thr	Asp	Lys
	165					170			175						
Gly	Gln	Val	Ile	Asp	Ala	Asn	Met	Val	Glu	Gly	Thr	Ala	Tyr	Leu	Ser
	180					185			190						
Ser	Phe	Leu	Trp	Lys	Thr	Gln	Lys	Ser	Ser	Leu	Trp	Glu	Ala	Pro	Arg
	195					200			205						

Gly Gln Asn Met Leu Asp Gly Gly Ala Pro Phe Tyr Thr Thr Tyr Arg
 210 215 220
 Thr Ala Asp Gly Glu Phe Met Ala Val Gly Ala Ile Glu Pro Gln Phe
 225 230 235 240
 Tyr Glu Leu Leu Ile Lys Gly Leu Gly Leu Lys Ser Asp Glu Leu Pro
 245 250 255
 Asn Gln Met Ser Met Asp Asp Trp Pro Glu Met Lys Lys Lys Phe Ala
 260 265 270
 Asp Val Phe Ala Lys Lys Thr Lys Ala Glu Trp Cys Gln Ile Phe Asp
 275 280 285
 Gly Thr Asp Ala Cys Val Thr Pro Val Leu Thr Phe Glu Glu Val Val
 290 295 300
 His His Asp His Asn Lys Glu Arg Gly Ser Phe Ile Thr Ser Glu Glu
 305 310 315 320
 Gln Asp Val Ser Pro Arg Pro Ala Pro Leu Leu Leu Asn Thr Pro Ala
 325 330 335
 Ile Pro Ser Phe Lys Arg Asp Pro Phe Ile Gly Glu His Thr Glu Glu
 340 345 350
 Ile Leu Glu Phe Gly Phe Ser Arg Glu Glu Ile Tyr Gln Leu Asn
 355 360 365
 Ser Asp Lys Ile Ile Glu Ser Asn Lys Val Lys Ala Ser Leu
 370 375 380

(2) INFORMATION FOR SEQ ID NO:109:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1524 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:109:

GGCACGAGGC	TGCGCCAGGG	CCTGAGCGGA	GGCGGGGGCA	GCCTCGCCAG	CGGGGGCCCC	60
GGGCCTGGCC	ATGCCCTACT	GAGCCAGCGC	CTGCGCCTCT	ACCTCGCCGA	CAGCTGAAAC	120
CAGTGCACC	TAGTGGCTCT	CACCTGCTTC	CTCCTGGCG	TGGGCTGCCG	GCTGACCCCG	180
GGTTTGACCC	ACCTGGGCCG	CACTGTCCTC	TGCATCGACT	TCATGGTTTT	CACGGTGCAG	240
CTGCTTCACA	TCTTCACCGT	CAACAAACAG	CTGGGGCCA	AGATCGTCAT	CGTGAGCAAG	300
ATGATGAAGG	ACGTGTTCTT	CTTCCTCTTC	TTCCCTCGGC	TGTGGCTGGT	AGCCTATGGC	360
GTGGCCACGG	AGGGGCTCCT	GAGGCCACGG	GACAGTGA	TCCAAGTAT	CCTGCGCCGC	420
GTCTTCTACC	GTCCCCTACCT	GCAGATCTTC	GGGCAGATT	CCCAGGAGGA	CATGGACGTG	480
GCCCTCATGG	AGCACAGCAA	CTGCTCGTC	GAGCCCGGCT	TCTGGCACA	CCCTCCTGGG	540
GCCCAGCGG	GCACCTCGGT	CTCCCAGTAT	GCCAACTGGC	TGGTGGTGC	GCTCCTCGTC	600
ATCTTCCCTGC	TCGTGGCCAA	CATCCTGCTG	GTCAACTTGC	TCATTGCCAT	GTTCAAGTTAC	660
ACATTGGCA	AAAGTACAGGG	CAACAGCGAT	CTCTACTGG	AGGCGCAGCG	TTACCGCCCTC	720
ATCCGGGAAT	TCCACTCTCG	GCCCCGGCTG	GCCCCGCCCT	TTATCGTCAT	CTCCCACTTG	780
CGCCTCCCTGC	TCAGGCAATT	GTGCAGGCCA	CCCCGGAGCC	CCCAGCGTC	CTCCCCGGCC	840
CTCGAGCATT	TCCGGGTTTA	CCTTCTAACG	GAAGCCGAGC	GGAAAGCTGCT	AACGTGGAA	900
TCGGTGCATA	AGGAGAACTT	TCTGCTGGCA	CGCGCTAGGG	ACAAGCGGGA	GAGCGACTCC	960
GAGCGTCTGA	AGCGCACGTC	CCAGAACGGT	GACTTGGCAC	TGAAACAGCT	GGGACACATC	1020
CGCGAGTACG	AAACAGCGCCT	GAAAGTGTG	GAGCAGGGAGG	TCCAGCAGTG	TAGCCCGTC	1080
CTGGGGTGGG	TGGCCGAGGC	CCTGAGCCGC	TCTGCCTTGC	TGCCCGCAGG	TGGGCCGCCA	1140
CCCCCTGACC	TGCCTGGGTC	CAAAGACTGA	GCCCTGCTGG	CGGACTTCAA	GGAGAACGCC	1200
CCACAGGGGA	TTTGCTCCT	AGAGTAAGGC	TCATCTGGGC	CTCGGCCCCC	GCACCTGGTG	1260
GCCTTGTCCCT	TGAGGTGAGC	CCCATGTCCA	TCTGGGCCAC	TGTCAAGGACC	ACCTTTGGGA	1320
GTGTCATCCT	TACAAACCAC	AGCATGCCCG	GCTCCTCCCA	GAACCAGTCC	CAGCCTGGGA	1380

GGATCAAGGC CTGGATCCCG GGCCGTTATC CATCTGGAGG CTGCAGGGTC CTTGGGGTAA	1440
CAGGGACAC AGACCCCCTCA CCACTCACAG ATTCTACA CTGGGGAAAT AAAGCCATT	1500
CAGAGGAAAA AAAAAAAA AAAA	1524

(2) INFORMATION FOR SEQ ID NO:110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 3410 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:110:

GGAAACCAGC CTGCACGCGC TGGCTCCGGG TGACAGCCCC GCGCCTCGGC CAGGATCTGA	60
GTGATGAGAC GTGTCCCCAC TGAGGTGCC CACAGCAGCA GGTGTTGAGC ATGGGCTGAG	120
AAGCTGGACC GGCACCAAAG GGCTGGCAGA AATGGGCGCC TGGCTGATTC CTAGGCAGTT	180
GGCGGCAGCA AGGAGGAGAG GCGCGAGCTT CTGGAGCAGA GCGCAGACGA AGCAGTTCTG	240
GAGTGCCCTGA ACGGCCCCCT GAGCCCTACC CGCCTGGCCC ACTATGGTCC AGAGGCTGTG	300
GGTGAGCCGC CTGCTGCCGC ACCGGAAAGC CCAGCTCTTG CTGGTCAACC TGCTAACCTT	360
TGGCCTGGAG GTGTGTTTGG CCGCAGGCAT CACCTATGTG CCGCCTCTGC TGCTGGAAGT	420
GGGGTAGAG GAGAAGTTCA TGACCATGGT GCTGGCATT GGTCAGTGC TGGGCTGGT	480
CTGTGTCCCCT CTCCCTAGGCT CAGCCAGTGA CCACTGGCGT GGACGCTATG GCCGCCGCC	540
GCCCTTCATC TGGGCACTGT CCTGGGCAT CCTGCTGAGC CTCTTCTCA TCCAAGGGC	600
CGGCTGGCTA GCAGGGCTG TGTGCCCCGA TCCCAGGGC CTGGAGCTGG CACTGCTCAT	660
CCTGGGCGTG GGGCTGCTGG ACTTCTGTGG CCAGGTGTGC TTCACTCCAC TGGAGGCCCT	720
GCTCTCTGAC CTCTTCCGGG ACCCGGACCA CTGTCGCCAG GCCTACTCTG TCTATGCCTT	780
CATGATCAGT CTGGGGGCT GCCTGGCTA CCTCTGCTC GCCATTGACT GGGACACCA	840
TGCCCTGGCC CCTTACCTGG GCACCCAGGA GGAGTGCCTC TTTGGCCTGC TCACCCCTCAT	900
CTTCTCTACC TCGTAGCAG CCACACTGCT GGTGGCTGAG GAGGCAGCGC TGGGCCAAC	960
CGAGCCAGCA GAAGGGCTGT CGGCCCCCTC CTTGTCGCC CACTGCTGTC CATGCCGGC	1020
CCGCTTGCT TTCCGGAAACC TGGGCGCCCT GCTTCCCCGG CTGCACCAGC TGTGCTGCCG	1080
CATGCCCGC ACCCTGCGCC GGCTCTTCGT GGCTGAGCTG TGCAGCTGGA TGGCACTCAT	1140
GACCTTCACG CTGTTTACA CGGATTTCTG GGGCGAGGGG CTGTACCAGG GCGTGCCAG	1200
AGCTGAGCCG GGCACCGAGG CCCGGAGACA CTATGATGAA GGCCTTCGGA TGGGCAGCCT	1260
GGGGCTGTTG CTGCACTGCG CCATCTCCCT GGTCTTCTCT CTGGTCATGG ACCGGCTGGT	1320
GCAGCGATTC GGCACTCGAG CAGTCTATTT GGCCAGTGTG GCAGCTTTCC CTGTGGCTGC	1380
CGGTGCCACA TGCCCTGTCAC ACAGTGTGCG CGTGGTGACA GCTTCAGCCG CCCTCACCGG	1440
GTTCACCTTC TCAGCCCTGC AGATCTCTCC CTACACACTG GCCTCCCTCT ACCACCGGG	1500
GAAGCAGGTG TTCCCTGCCA AATACCGAGG GGACACTGGA GGTGCTAGCA GTGAGGACAG	1560
CCTGATGACC AGCTTCTTCG CAGGCCCTAA GCCTGGAGCT CCCTCCCTA ATGGACACGT	1620
GGGTGCTGGA GGCAGTGGCC TGCTCCACC TCCACCCGGC CTCTGGGGG CCTCTGCCTG	1680
TGATGCTCTC GTACGTGTGG TGGTGGGTGA GCCCCACCGAG GCCAGGGTGG TTCCGGGCCG	1740
GGGCATCTGC CTGGACCTCG CCATCTGGA TAGTGCCTTC CTGCTGCTCC AGGTGGCCCC	1800
ATCCCTGTTT ATGGCTCCA TTGTCCAGCT CAGCCAGTCT GTCACTGCCT ATATGGTGT	1860
TGCGCAGGC CTGGGTCTGG TCGCCATTAA CTTTGTACA CAGGTAGTAT TTGACAAGAG	1920
CGACTTGGCC AAATACTCAG CGTAGAAAC TTCCAGCACA TTGGGGTGGA GGGCCTGCCT	1980
CACTGGGTCC CAGCTCCCCG CTCCCTGTTAG CCCCCATGGGG CTGCCGGGGCT GGCGGCCAGT	2040
TTCTGTTGCT GCCAAAGTAA TGTGGCTCTC TGCTGCCACC CTGTGCTGCT GAGGTGCGTA	2100
GCTGCACAGC TGGGGCTGG GCGCTCCCTC TCCTCTCTCC CCAGTCTCTA GGGCTGCCTG	2160
ACTGGAGGCC TTCAAGGGGG GTTTCAGTCT GGACTTATAC AGGGAGGCCA GAAGGGCTCC	2220
ATGCACCTGGA ATGCGGGGAC TCTGCAGGTG GATTACCCAG GCTCAGGGTT AACAGCTAGC	2280
CTCCTAGTTG AGACACACCT AGAGAAGGGT TTTTGGGAGC TGAATAAAACT CAGTCACCTG	2340
GTTCCTCCATC TCTAACGCCCC TTAACCTGCA GCTTCGTTTA ATGTAGCTCT TGCAATGGGAG	2400
TTTCAGGAT GAAACACTCC TCCATGGGAT TTGAACATAT GACTTATTG TAGGGGAAGA	2460
GTCCTGAGGG GCAACACACCA AGAACCAAGGT CCCCTCAGCC CACAGCACTG TCTTTTGCT	2520

GATCCACCCC CCTCTTACCT TTTATCAGGA TGTGGCCTGT TGGTCCTTCT GTGCCATCA	2580
CAGAGACACA GGCATTAAA TATTTAACCT ATTTATTTAA CAAAGTAGAA GGGATCCAT	2640
TGCTAGCTT TCTGTGTTGG TGTCTAATAT TTGGGTAGGG TGGGGATCC CCAACAATCA	2700
GGTCCCCCTGA GATAGCTGGT CATTGGCTG ATCATGCCA GAATCTTCTT CTCCTGGGT	2760
CTGGCCCCC AAAATGCCA ACCCAGGACC TTGAAATTCTACTCATCCC AAATGATAAT	2820
TCCAATGCT GTTACCCAAG GTTGGGTGT TGAAGGAAGG TAGAGGGTGG GGCTTCAGGT	2880
CTCAACGGCT TCCCTAACCA CCCCTTCTCT CTTGGCCAG CCTGGTCCCC CCCACTTCCA	2940
CTCCCTCTA CTCTCTCTAG GACTGGCTG ATGAAGGCAC TGCCCAAAT TTCCCTTACC	3000
CCCAACTTTC CCCTACCCCC AACTTCCCC ACCAGCTCCA CAACCTGTT TGGAGCTACT	3060
GCAGGACCAG AAGCACAAAG TGCGGTTTC CAAGCCTTG TCCATCTCAG CCCCCAGAGT	3120
ATATCTGTGC TTGGGAATC TCACACAGAA ACTCAGGAGC ACCCCCTGCC TGAGCTAAGG	3180
GAGGTCTTAT CTCTCAGGGG GGGTTTAAGT GCGTTTGCA ATAATGTCGT CTTATTTATT	3240
TAGGGGGTG AATATTTAT ACTGTAAGTG AGCAATCAGA GTATAATGTT TATGGTGACA	3300
AAATTAAAGG CTTCTTATA TGTTAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA	3360
AAAAAAAAA AAAAAAAAAA AAAAAAATAA AAAAAAAAAA	3410

(2) INFORMATION FOR SEQ ID NO:111:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1289 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:111:

AGCCAGGCGT CCCTCTGCCT GCCCACTCAG TGGCAACACC CGGGAGCTGT TTTGTCCTT	60
GTGGAGCCTC AGCAGTCCC TCTTCAGAA CTCACTGCCA AGAGCCTGA ACAGGAGCCA	120
CCATGCAGTG CTTCAGCTTC ATTAAGACCA TGATGATCCT CTCATCTTTC	180
TGTGTGGTGC AGCCCTGTTG GCAGTGGCA TCTGGTGTG AACATGGGG GCATCCTTTC	240
TGAAGATCTT CGGGCCACTG TCGTCCAGTG CCATCCAGTT TGTCAACGTG GGCTACTTCC	300
TCATCGCAGC CGGCCTTGTG GTCTTGCTC TTGGTTCCCT GGGCTGCTAT GGTGCTAAGA	360
CTGAGAGCAA GTGTGCCCTC GTGACGTTCT TCTTCATCCT CCTCCATC TTCATTGCTG	420
AGGTTGCAGC TGCTGTGGTC GCCTGGTGT ACACCACAAT GGCTGAGCAC TTCCCTGACGT	480
TGCTGGTAGT GCCTGCCATC AAGAAAGATT ATGGTTCCA GGAAGACTTC ACTCAAGTGT	540
GGAACACCAC CATGAAAGGG CTCAAGTGC GTGGCTTCAC CAACTATACG GATTTTGAGG	600
ACTCACCCCTA CTTCAAAGAG AACAGTGCCT TTCCCCATT CTGTTGCAAT GACAACGTCA	660
CCAACACAGC CAATGAAACC TGCACCAAGC AAAAGCTCA CGACCAAAAAA GTAGAGGGTT	720
GCTTCAATCA GCTTTTGAT GACATCCGAA CTAATGCACT CACCGTGGGT GGTGTGGCAG	780
CTGGAATTGG GGGCCTCGAG CTGGCTGCCA TGATGATGTC CATGTATCTG TACTGCAATC	840
TACAATAAGT CCACCTCTGC CTCTGCCACT ACTGCTGCCA CATGGGAACG GTGAAGAGGC	900
ACCCCTGGCAA GCAGCAGTGA TTGGGGAGG GGACAGGATC TAACAATGTC ACTTGGGCCA	960
GAATGGACCT GGGCTTCTG CTCCAGACCT GGGGTAGAT AGGGACCACT CCTTTTAGCG	1020
ATGCCCTGACT TTCCCTTCCAT TTGGGGTGG ATGGGGGGG GGCATTCAG AGCCTCTAAG	1080
GTAGCCAGTT CTGTTGCCA TTCCCCCAGT CTATTAACC CTTGATATGC CCCCTAGGCC	1140
TAGTGGTGTAT CCCAGTGCTC TACTGGGGGA TGAGAGAAAG GCATTTATA GCCTGGCAT	1200
AAGTGAATC AGCAGAGCCT CTGGGTGGAT GTGTAGAAGG CACTTCAAAA TGCATAAAC	1260
TGTTACAATG TTAAAAAAA AAAAAAAAAA	1289

(2) INFORMATION FOR SEQ ID NO:112:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:

Met Val Phe Thr Val Arg Leu Leu His Ile Phe Thr Val Asn Lys Gln
1 5 10 15

Leu Gly Pro Lys Ile Val Ile Val Ser Lys Met Met Lys Asp Val Phe
20 25 30

Phe Phe Leu Phe Phe Leu Gly Val Trp Leu Val Ala Tyr Gly Val Ala
35 40 45

Thr Glu Gly Leu Leu Arg Pro Arg Asp Ser Asp Phe Pro Ser Ile Leu
50 55 60

Arg Arg Val Phe Tyr Arg Pro Tyr Leu Gln Ile Phe Gly Gln Ile Pro
65 70 75 80

Gln Glu Asp Met Asp Val Ala Leu Met Glu His Ser Asn Cys Ser Ser
85 90 95

Glu Pro Gly Phe Trp Ala His Pro Pro Gly Ala Gln Ala Gly Thr Cys
100 105 110

Val Ser Gln Tyr Ala Asn Trp Leu Val Val Leu Leu Val Ile Phe
115 120 125

Leu Leu Val Ala Asn Ile Leu Leu Val Asn Leu Leu Ile Ala Met Phe
130 135 140

Ser Tyr Thr Phe Gly Lys Val Gln Gly Asn Ser Asp Leu Tyr Trp Lys
145 150 155 160

Ala Gln Arg Tyr Arg Leu Ile Arg Glu Phe His Ser Arg Pro Ala Leu
165 170 175

Ala Pro Pro Phe Ile Val Ile Ser His Leu Arg Leu Leu Arg Gln
180 185 190

Leu Cys Arg Arg Pro Arg Ser Pro Gln Pro Ser Ser Pro Ala Leu Glu
195 200 205

His Phe Arg Val Tyr Leu Ser Lys Glu Ala Glu Arg Lys Leu Leu Thr
210 215 220

Trp Glu Ser Val His Lys Glu Asn Phe Leu Leu Ala Arg Ala Arg Asp
225 230 235 240

Lys Arg Glu Ser Asp Ser Glu Arg Leu Lys Arg Thr Ser Gln Lys Val
245 250 255

Asp Leu Ala Leu Lys Gln Leu Gly His Ile Arg Glu Tyr Glu Gln Arg
260 265 270

Leu Lys Val Leu Glu Arg Glu Val Gln Gln Cys Ser Arg Val Leu Gly
275 280 285

Trp Val Ala Glu Ala Leu Ser Arg Ser Ala Leu Leu Pro Pro Gly Gly
 290 295 300

Pro Pro Pro Pro Asp Leu Pro Gly Ser Lys Asp
 305 310 315

(2) INFORMATION FOR SEQ ID NO:113:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 553 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:

Met Val Gln Arg Leu Trp Val Ser Arg Leu Leu Arg His Arg Lys Ala
 1 5 10 15

Gln Leu Leu Leu Val Asn Leu Leu Thr Phe Gly Leu Glu Val Cys Leu
 20 25 30

Ala Ala Gly Ile Thr Tyr Val Pro Pro Leu Leu Leu Glu Val Gly Val
 35 40 45

Glu Glu Lys Phe Met Thr Met Val Leu Gly Ile Gly Pro Val Leu Gly
 50 55 60

Leu Val Cys Val Pro Leu Leu Gly Ser Ala Ser Asp His Trp Arg Gly
 65 70 75 80

Arg Tyr Gly Arg Arg Pro Phe Ile Trp Ala Leu Ser Leu Gly Ile
 85 90 95

Leu Leu Ser Leu Phe Leu Ile Pro Arg Ala Gly Trp Leu Ala Gly Leu
 100 105 110

Leu Cys Pro Asp Pro Arg Pro Leu Glu Leu Ala Leu Ile Leu Gly
 115 120 125

Val Gly Leu Leu Asp Phe Cys Gly Gln Val Cys Phe Thr Pro Leu Glu
 130 135 140

Ala Leu Leu Ser Asp Leu Phe Arg Asp Pro Asp His Cys Arg Gln Ala
 145 150 155 160

Tyr Ser Val Tyr Ala Phe Met Ile Ser Leu Gly Gly Cys Leu Gly Tyr
 165 170 175

Leu Leu Pro Ala Ile Asp Trp Asp Thr Ser Ala Leu Ala Pro Tyr Leu
 180 185 190

Gly Thr Gln Glu Glu Cys Leu Phe Gly Leu Leu Thr Leu Ile Phe Leu
 195 200 205

Thr Cys Val Ala Ala Thr Leu Leu Val Ala Glu Glu Ala Ala Leu Gly
 210 215 220

Pro Thr Glu Pro Ala Glu Gly Leu Ser Ala Pro Ser Leu Ser Pro His
 225 230 235 240

Cys Cys Pro Cys Arg Ala Arg Leu Ala Phe Arg Asn Leu Gly Ala Leu
 245 250 255

Leu Pro Arg Leu His Gln Leu Cys Cys Arg Met Pro Arg Thr Leu Arg
 260 265 270

Arg Leu Phe Val Ala Glu Leu Cys Ser Trp Met Ala Leu Met Thr Phe
 275 280 285

Thr Leu Phe Tyr Thr Asp Phe Val Gly Glu Gly Leu Tyr Gln Gly Val
 290 295 300

Pro Arg Ala Glu Pro Gly Thr Glu Ala Arg Arg His Tyr Asp Glu Gly
 305 310 315 320

Val Arg Met Gly Ser Leu Gly Leu Phe Leu Gln Cys Ala Ile Ser Leu
 325 330 335

Val Phe Ser Leu Val Met Asp Arg Leu Val Gln Arg Phe Gly Thr Arg
 340 345 350

Ala Val Tyr Leu Ala Ser Val Ala Ala Phe Pro Val Ala Ala Gly Ala
 355 360 365

Thr Cys Leu Ser His Ser Val Ala Val Val Thr Ala Ser Ala Ala Leu
 370 375 380

Thr Gly Phe Thr Phe Ser Ala Leu Gln Ile Leu Pro Tyr Thr Leu Ala
 385 390 395 400

Ser Leu Tyr His Arg Glu Lys Gln Val Phe Leu Pro Lys Tyr Arg Gly
 405 410 415

Asp Thr Gly Gly Ala Ser Ser Glu Asp Ser Leu Met Thr Ser Phe Leu
 420 425 430

Pro Gly Pro Lys Pro Gly Ala Pro Phe Pro Asn Gly His Val Gly Ala
 435 440 445

Gly Gly Ser Gly Leu Leu Pro Pro Pro Ala Leu Cys Gly Ala Ser
 450 455 460

Ala Cys Asp Val Ser Val Arg Val Val Val Gly Glu Pro Thr Glu Ala
 465 470 475 480

Arg Val Val Pro Gly Arg Gly Ile Cys Leu Asp Leu Ala Ile Leu Asp
 485 490 495

Ser Ala Phe Leu Leu Ser Gln Val Ala Pro Ser Leu Phe Met Gly Ser
 500 505 510

Ile Val Gln Leu Ser Gln Ser Val Thr Ala Tyr Met Val Ser Ala Ala
 515 520 525

Gly Leu Gly Leu Val Ala Ile Tyr Phe Ala Thr Gln Val Val Phe Asp

530	535	540
Lys Ser Asp Leu Ala Lys Tyr Ser Ala		
545	550	
(2) INFORMATION FOR SEQ ID NO:114:		
(i) SEQUENCE CHARACTERISTICS:		
(A) LENGTH: 241 amino acids		
(B) TYPE: amino acid		
(C) STRANDEDNESS: single		
(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: protein		
(vi) ORIGINAL SOURCE:		
(A) ORGANISM: Homo sapiens		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:		
Met Gln Cys Phe Ser Phe Ile Lys Thr Met Met Ile Leu Phe Asn Leu		
1	5	10
Leu Ile Phe Leu Cys Gly Ala Ala Leu Leu Ala Val Gly Ile Trp Val		
20	25	30
Ser Ile Asp Gly Ala Ser Phe Leu Lys Ile Phe Gly Pro Leu Ser Ser		
35	40	45
Ser Ala Met Gln Phe Val Asn Val Gly Tyr Phe Leu Ile Ala Ala Gly		
50	55	60
Val Val Val Phe Ala Leu Gly Phe Leu Gly Cys Tyr Gly Ala Lys Thr		
65	70	75
Glu Ser Lys Cys Ala Leu Val Thr Phe Phe Ile Leu Leu Ile		
85	90	95
Phe Ile Ala Glu Val Ala Ala Val Val Ala Leu Val Tyr Thr Thr		
100	105	110
Met Ala Glu His Phe Leu Thr Leu Leu Val Val Pro Ala Ile Lys Lys		
115	120	125
Asp Tyr Gly Ser Gln Glu Asp Phe Thr Gln Val Trp Asn Thr Thr Met		
130	135	140
Lys Gly Leu Lys Cys Cys Gly Phe Thr Asn Tyr Thr Asp Phe Glu Asp		
145	150	155
160		
Ser Pro Tyr Phe Lys Glu Asn Ser Ala Phe Pro Pro Phe Cys Cys Asn		
165	170	175
Asp Asn Val Thr Asn Thr Ala Asn Glu Thr Cys Thr Lys Gln Lys Ala		
180	185	190
His Asp Gln Lys Val Glu Gly Cys Phe Asn Gln Leu Leu Tyr Asp Ile		
195	200	205
Arg Thr Asn Ala Val Thr Val Gly Gly Val Ala Ala Gly Ile Gly Gly		
210	215	220

Leu Glu Leu Ala Ala Met Ile Val Ser Met Tyr Leu Tyr Cys Asn Leu
 225 230 235 240

Gln

(2) INFORMATION FOR SEQ ID NO:115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo Sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:

GCTCTTCCTC TCCCCTCCTC TGAATTTAAT TCTTCAACT TGCAATTTGC AAGGATTACA	60
CATTTCACTG TGATGTATAT TGTGTTGCAA AAAAAAAA GTGCTTTGT TTAAATTAC	120
TTGGTTTGTG AATCCATCTT GCTTTTCCC CATTGGAAC AGTCATTAAC CCATCTCTGA	180
ACTGGTAGAA AAACATCTGA AGAGCTAGTC TATCAGCATC TGACAGGTGA ATTGGATGGT	240
TCTCAGAACC ATTTCACCCA GACAGCTGT TTCTATCCTG TTTAATAAAT TAGTTGGGT	300
TCTCTACATG CATAACAAAC CCTGCTCCAA TCTGTCACAT AAAAGTCTGT GACTTGAAAGT	360
TTAGTC	366

(2) INFORMATION FOR SEQ ID NO:116:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 282 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:

ACAAAGATGA ACCATTCCT ATATTATAGC AAAATAAAAA TCTACCGTA TTCTAATATT	60
GAGAAATGAG ATNAAACACA ATNTTATAAA GTCTACTTAG AGAAGATCAA GTGACCTCAA	120
AGACTTTACT ATTTCATAT TTTAAGACAC ATGATTATC CTATTTAGT AACCTGGTTC	180
ATACGTTAAA CAAAGGATAA TGTGAACAGC AGAGAGGATT TGTGGCAGA AAATCTATGT	240
TCAATCTNGA ACTATCTANA TCACAGACAT TTCTATTCCCT TT	282

(2) INFORMATION FOR SEQ ID NO:117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 305 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:117:

ACACATGTCG CTTCACTGCC TTCTTAGATG CTTCTGGTCA ACATANAGGA ACAGGGACCA	60
TATTTATCCT CCCTCCTGAA ACAATTGCAA AATAANACAA AATATATGAA ACAATTGCAA	120
AATAAGGCAA AATATATGAA ACAACAGGTC TCGAGATATT GGAAATCAGT CAATGAAGGA	180
TACTGATCCC TGATCACTGT CCTAATGCAG GATGTGGAA ACAGATGAGG TCACCTCTGT	240
GACTGCCCA GCTTACTGCC TGTAGAGAGT TTCTANGCTG CAGTTCAGAC AGGGAGAAAT	300
TGGGT	305

(2) INFORMATION FOR SEQ ID NO:118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:

ACCAAGGTGT NTGAATCTCT GACGTGGGA TCTCTGATTCCCGCACAAATCTGAGTGAAA	60
AANTCCTGGG T	71

(2) INFORMATION FOR SEQ ID NO:119:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:119:

ACTCCGGTTG GTGTCAGCAG CACGTGGCAT TGAACATNGC AATGTGGAGC CCAAACCACA	60
GAAAATGGGG TGAATTGGC CAACTTCTA TNAACTTATG TTGGCAANTT TGCCACCAAC	120
AGTAAGCTGG CCCTTCTAAT AAAAGAAAAT TGAAAGGTTT CTCACTAANC GGAATTAANT	180
AATGGANTCA AGANACTCCC AGGCCTCAGC GT	212

(2) INFORMATION FOR SEQ ID NO:120:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 90 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:120:

ACTCGTTGCA NATCAGGGC CCCCCAGAGT CACCGTTGCA GGAGTCCTTC TGGTCTTGCC	60
CTCCGCCGGC GCAGAACATG CTGGGGTGGT	90

(2) INFORMATION FOR SEQ ID NO:121:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:

TGTANC GTGA ANACGACAGA NAGGGTTGTC AAAATGGAG AANCCTTGAA GTCATTTGA	60
GAATAAGATT TGCTAAAAGA TTTGGGGCTA AAACATGGTT ATTGGGAGAC ATTTCTGAAG	120
ATATNCANGT AAATTANGGA ATGAATTCAT GGTTCTTTG GGAATTCCCTT TACGATNGCC	180
AGCATANACT TCATGTGGGG ATANCAGCTA CCCTTGTA	218

(2) INFORMATION FOR SEQ ID NO:122:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:

TAGGGGTGTA TGCAACTGTA AGGACAAAAA TTGAGACTCA ACTGGCTTAA CCAATAAAGG	60
CATTGTTAG CTCATGGAAC AGGAAGTCGG ATGGTGGGGC ATCTTCAGTG CTGCATGAGT	120
CACCACCCCG GCGGGGTCAT CTGTGCCACA GGTCCCTGTT GACAGTGCAGG T	171

(2) INFORMATION FOR SEQ ID NO:123:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 76 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:123:

TGTAGCGTGA AGACNACAGA ATGGTGTGTG CTGTGCTATC CAGGAACACA TTTATTATCA TTATCAANTA TTGTGT	60 76
----------------------------------------------------------------------------------------	----------

(2) INFORMATION FOR SEQ ID NO:124:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 131 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:124:

ACCTTTCCCC AAGGCCAATG TCCTGTGTGC TAACTGGCCG GCTGCAGGAC AGCTGCAATT CAAATGCTG GGTCAATATGG AGGGGAGGAG ACTCTAAAAT AGCCAATTTT ATTCTCTTGG TTAAGATTTG T	60 120 131
--------------------------------------------------------------------------------------------------------------------------------------------------------	------------------

(2) INFORMATION FOR SEQ ID NO:125:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:

ACTTTATCTA CTGGCTATGA AATAGATGGT GGAAAATTGC GTTACCAACT ATACCACTGG CTTGAAAAAG AGGTGATAGC TCTTCAGAGG ACTTGTGACT TTTGCTCAGA TGCTGAAGAA CTACAGTCTG CATTGGCAG AAATGAAGAT GAATTTGGAT TAAATGAGGA TGCTGAAGAT TTGCTTCACC AAACAAAAGT GAAACAACTG AGAGAAAATT TTCAGGAAAA AAGACAGTGG CTCTTGAAGT ATCAGTCACT TTTGAGAATG TTTCTTAGTT ACTGCATACT TCATGGATCC CATGGTGGGG GTCTTGCATC TGTAAGAATG GAATTGATTT TGCTTTGCA AGAACATCTCAG CAGGAAACAT CAGAACCACT ATTTTCTAGC CCTCTGTCAG AGCAAACCTC AGTGCCTCTC CTCTTGCTT GT	60 120 180 240 300 360 420 432
-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	-----------------------------------------------------

(2) INFORMATION FOR SEQ ID NO:126:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 112 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:

ACACAACCTG AATAGTAAAA TAGAACTGA GCTGAAATT CTAATTCACT TTCTAACCAT AGTAAGAATG ATATTCCCC CCAGGGATCA CCAAATATT GT	60 112
-----------------------------------------------------------------------------------------------------------------	-----------

(2) INFORMATION FOR SEQ ID NO:127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 54 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:

ACCACGAAAC CACAAACAAG ATGGAAGCAT CAATCCACTT GCCAAGCACA GCAG	54
-------------------------------------------------------------	----

(2) INFORMATION FOR SEQ ID NO:128:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 323 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:

ACCTCATTAG TAATTGTTTT GTGTTTCAT TTTTTCTAA TGCTCCCCCT CTACCAGCTC ACCTGAGATA ACAGAATGAA AATGGAAGGA CAGCCAGATT TCTCCTTGCG TCTCTGCTCA TTCTCTCTGA AGTCTAGGTT ACCCATTGGT GGGACCCATT ATAGGCAATA AACACAGTTC CCAAAGCATT TGGACAGTTT CTTGTTGTGT TTTAGAATGG TTTTCCTTTT TCTTAGCCTT TTCCTGCAAA AGGCTCACTC AGTCCCTTGC TTGCTCAGTG GACTGGGCTC CCCAGGGCCT AGGCTGCCTT CTTTCCATG TCC	60 120 180 240 300 323
---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------	---------------------------------------

(2) INFORMATION FOR SEQ ID NO:129:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:

ACATACATGT GTGTATATTT TTAAATATCA CTTTGTATC ACTCTGACTT TTTAGCATACT TGAAAACACA CTAACATAAT TTNTGTGAAC CATGATCAGA TACAACCCAA ATCATTCACT	60 120
----------------------------------------------------------------------------------------------------------------------------------------	-----------

TAGCACATTC ATCTGTGATA NAAAGATAGG TGAGTTCAT TTCCCTTCACG TTGGCCAATG	180
GATAAACAAA GT	192

(2) INFORMATION FOR SEQ ID NO:130:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 362 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:

CCCTTTTTTA TGGAATGAGT AGACTGTATG TTTGAANATT TANCCACAAC CTCTTTGACA	60
TATAATGACG CAAACAAAAAG GTGCTGTTA GTCCTATGGT TCAGTTTATG CCCCTGACAA	120
GTTTCCATTG TGTGTTGCCG ATCTTCTGGC TAATCGGGT ATCTCTCCATG TTATTAGTAA	180
TTCTGTATTG CATTGTTGTTA ACGCCTGGTA GATGTAACCT GCTANGAGGC TAACTTTATA	240
CTTAAATTAAA AGCTCTTATT TTGTGGTCAT TAAAATGGCA ATTATATGTGC AGCACCTTAT	300
TGCAGCAGGA AGCACGTGTG GGTTGGTTGT AAAGCTCTTA GCTAATCTTA AAAAGTAATG	360
GG	362

(2) INFORMATION FOR SEQ ID NO:131:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 332 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:

CTTTTGAAA GATCGTGTCC ACTCCTGTGG ACATCTTGTGTT TTAATGGAGT TTCCCATGCA	60
GTANGACTGG TATGGTTGCA GCTGTCAGA TAAAACATT TGAAGAGCTC CAAATGAGA	120
GTTCTCCCAG GTTCGCCCTG CTGCTCCAAG TCTCAGCAGC AGCTCTTTT AGGAGGCATC	180
TTCTGAACTA GATTAAGGCA GCTTGTAAT CTGATGTGAT TTGGTTTATT ATCCAACCAA	240
CTTCATCTG TTATCACTGG AGAAAGCCA GACTCCCCAN GACNGGTACG GATTGTGGGC	300
ATANAAGGAT TGGGTGAAGC TGGCGTTGTG GT	332

(2) INFORMATION FOR SEQ ID NO:132:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 322 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:

ACTTTGCCA	TTTGTTATAT	ATAAAACAATC	TTGGGACATT	CTCCTGAAAA	CTAGGTGTCC	60
AGTGGCTAAG	AGAAACTCGAT	TTCAAGCAAT	TCTGAAAGGA	AAACCAGCAT	GACACAGAAAT	120
CTCAAATTCC	CAAACAGGGG	CTCTGTGGGA	AAAATGAGGG	AGGACCTTG	TATCTCGGGT	180
TTTAGCAAGT	TAAAATGAAN	ATGACAGGAA	AGGCTTATT	ATCAACAAAG	AGAAGAGTTG	240
GGATGCTTCT	AAAAAAAACT	TTGGTAGAGA	AAATAGGAAT	GCTNAATCCT	AGGGAAAGCCT	300
GTAACAATCT	ACAAATTGGTC	CA				322

(2) INFORMATION FOR SEQ ID NO:133:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 278 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:

ACAAGCCTTC	ACAAGTTTAA	CTAAATTGGG	ATTAATCTTT	CTGTANTTAT	CTGCATAATT	60
CTTGTTTTTC	TTTCCATCTG	GCTCCTGGGT	TGACAATTG	TGGAAACAAC	TCTATTGCTA	120
CTATTTAAA	AAAATCACAA	ATCTTCCCT	TTAAGCTATG	TTNAATTCAA	ACTATTCTG	180
CTATTCCGT	TTTGTCAAAG	AAATTATATT	TTTCAAATA	TGTNTATTTG	TTTGATGGGT	240
CCCACGAAAC	ACTAATAAAA	ACCAAGAGA	CCAGCCTG			278

(2) INFORMATION FOR SEQ ID NO:134:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 121 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:

GTTTANAAAA	CTTGTAGG	TCCATAGAGG	AAAGAATGTT	AAACTTTGTA	TTTTAAAAACA	60
TGATTCTCTG	AGGTTAAACT	TGGTTTCAA	ATGTTATT	TACTTGATT	TTGCTTTGG	120
T						121

(2) INFORMATION FOR SEQ ID NO:135:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 350 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:

ACTTANAACC ATGCCTAGCA CATCAGAAC	60
ATANAAAGTG GTGACTGGTT AAGCGTGC	120
AAACTTGATA CTTTGTTCT AAGTAGGAAC	180
GGGTGCCCGG CAACTCCCTGC AGCCGCTC	240
CCACCTCAAT CAAGCCCTGG GCCATGCTAC	300
TTCCCAAGGA TGCAAAGCCT GGTGCTCAAC	350
TCCTGGGCG TCAACTCAGT	

(2) INFORMATION FOR SEQ ID NO:136:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 399 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:

TGTACCGTGA AGACGACAGA AGTTGCATGG CAGGGACAGG GCAGGGCCGA	60
GCTGTGATTG TATCCGAATA NTCCCTGTGA GAAAAGATAA TGAGATGACG	120
GCAGACTTGT GTCTGCCTTC AANAAGCCAG ACAGGAAGGC CCTGCCTGCC	180
CCTGGCGGCC AGCCAGCCAG CCACAGGTGG GCTTCTTCCT TTTGTGGTGA	240
AAAAGTGCAG AGGCCAGGG TCAGGTGTNA GTGGGTANGT GACCATAAAA	300
TCCCAGGAAC CGGGCAGAAC GGCATCCCCA CCTACAGCCA GCATGCCAC	360
GGTGCAGANG GATGAAGCAG CCAGNTGTTG TGCTGTGGT	399

(2) INFORMATION FOR SEQ ID NO:137:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 165 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:

ACTGGTGTGG TNGGGGGTGA TGCTGGTGGT ANAAGTTGAN GTGACTTCAN GATGGTGTGT	60
GGAGGAAGTG TGTGAACGTA GGGATGTAGA NGTTTGGCC GTGCTAAATG AGCTTCGGGA	120
TTGGCTGGTC CCACTGGTGG TCACTGTCAT TGGTGGGTT CCTGT	165

(2) INFORMATION FOR SEQ ID NO:138:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 338 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:

ACTCACTGGA ATGCCACATT CACAACAGAA TCAGAGGTCT GTGAAAACAT TAATGGCTCC	60
TTAACTTCTC CAGTAAAGAAT CAGGGACTTG AAATGGAAAC GTTAACAGCC ACATGCCAA	120
TGCTGGGCAG TCTCCCATGC CTTCCACAGT GAAAGGGCTT GAGAAAAATC ACATCCAATG	180
TCATGTGTTT CCAGCCACAC CAAAAGGTGC TTGGGGTGGA GGGCTGGGG CATANANGGT	240
CANGCCTCAG GAAGCCTCAA GTTCCATTCA GCTTGCAC TGACATTCC CCATNTTTAA	300
AAAAACTGAT GCCTTTTTT TTTTTTTTG TAAAATTC	338

(2) INFORMATION FOR SEQ ID NO:139:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 382 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:

GGGAATCTTG GTTTTGGCA TCTGGTTGCG CTATAGCCGA GGCCACTTTG ACAGAACAAA	60
GAAAGGGACT TCGAGTAAGA AGGTGATTAA CAGCCAGCCT AGTGCCTGAA GTGAAGGAGA	120
ATTCAAACAG ACCTCGTCAT TCCTGGTGTG AGCCTGGTCG GCTCACCGCC TATCATCTGC	180
ATTTGCCTTA CTCAGGTGCT ACCGGACTCT GGCCCTGAT GTCTGTAGTT TCACAGGATG	240
CCTTATTTGT CTTCTACACC CCACAGGGCC CCCTACTTCT TCGGATGTGT TTTTAATAAT	300
GTCAGCTATG TGCCCCATCC CCCTTCATGC CCTCCCTCCC TTTCCTACCA CTGCTGAGTG	360
CCCTGGAAC TGTAAAGT GT.	382

(2) INFORMATION FOR SEQ ID NO:140:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 200 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:

ACCAANCTT CTTTCTGTT TGTTNGATTT TACTATAGGG GTTTNGCTTN TTCTAAANAT	60
ACTTTTCATT TAACANCTTT TGTTAAGTGT CAGGTGCAC TTGCTCCAT ANAATTATTG	120
TTTTCACATT TCAACTTGTA TGTGTTGTC TCTTANAGCA TTGGTGAAAT CACATATTG	180
ATATTCAAGCA TAAAGGAGAA	200

(2) INFORMATION FOR SEQ ID NO:141:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 335 base pairs
 (B) TYPE: nucleic acid

(C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:

ACTTTATTTT CAAAACACTC ATATGTTGCA AAAAACACAT AGAAAAATAA AGTTTGGTGG	60
GGGTGCTGAC TAAACCTCAA GTCACAGACT TTTATGTGAC AGATTGGAGC AGGGTTTGT	120
ATGCATGTAG AGAACCCAAA CTAATTATT AAACAGGATA GAAACAGGCT GTCTGGGTGA	180
AATGGTTCTG AGAACCATCC AATTCACTG TCAGATGTG ATANACTAGC TCTTCAGATG	240
TTTTCTACC AGTTCAGAGA TNGGTTAATG ACTANTTCCA ATGGGGAAAA AGCAAGATGG	300
ATTCACAAAC CAAGTAATT TAAACAAAGA CACTT	335

(2) INFORMATION FOR SEQ ID NO:142:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 459 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:

ACCAGGTTAA TATTGCCACA TATATCCTTT CCAATTGCGG GCTAAACAGA CGTGTATT	60
GGGTGTTTA AAAGAACCCC AGCTTAATAT CAAGAGAAAT TGTGACCTTT CATGGAGTAT	120
CTGATGGAGA AAACACTGAG TTTTGACAAA TCTTATTAA TTCAGATAGC AGTCTGATCA	180
CACATGGTCC ACAACACTC AAATAATAA TCAAATATNA TCAGATGTTA AAGATTGGTC	240
TTCAACACATC ATAGCCAATG ATGCCCGCT TGCCTATAAT CTCTCCGACA TAAAACCACA	300
TCAACACCTC AGTGGCCACC AAACCATTCA GCACAGCTTC CTTAACTGTG AGCTGTTGA	360
AGCTACCAAGT CTGAGCACTA TTGACTATNT TTTTCANGCT CTGAATAGCT CTAGGGATCT	420
CAGCANGGGT GGGAGGAACC AGCTCAACCT TGGCGTANT	459

(2) INFORMATION FOR SEQ ID NO:143:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 140 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:143:

ACATTTCCCT CCACCAAGTC AGGACTCCTG GCTTCTGTGG GAGTTCTTAT CACCTGAGGG	60
AAATCCAAAC AGTCTCTCCT AGAAAGGAAT AGTGTACCA ACCCCACCCA TCTCCCTGAG	120
ACCATCCGAC TTCCCTGTGT	140

(2) INFORMATION FOR SEQ ID NO:144:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

ACTTCAGTAA CAACATACAA TAAACAACATT AAGTGTATAT TGCCATCTTT GTCATTTCT	60
ATCTATACCA CTCTCCCTTC TGAAAACAAN AATCACTANC CAATCACTTA TACAAATTG	120
AGGCAATTAA TCCATATTG TTTTCAATAA GGAAAAAAAG ATGT	164

(2) INFORMATION FOR SEQ ID NO:145:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 303 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:145:

ACGTAGACCA TCCAACCTTG TATTTGTAAT GGCAAACATC CAGNAGCAAT TCCTAACAA	60
ACTGGAGGGT ATTATACCC AATTATCCC TTCATTAACA TGCCCTCCTC CTCAGGCTAT	120
GCAGGACAGC TATCATAAGT CGGCCAGGC ATCCAGATAC TACCATTGAT ATAAACATTCA	180
GTAGGGGAGT CCATCCAAGT GACAGGTCTA ATCAAAGGAG GAAATGGAAC ATAAGCCCAG	240
TAGTAAAATN TTGCTTAGCT GAAACAGCCA CAAAAGACTT ACCGCCGTGG TGATTACCAT	300
CAA	303

(2) INFORMATION FOR SEQ ID NO:146:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 327 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:146:

ACTGCAGCTC ATTAGAAGT GGTCTCTGAC TTTCATCANC TTCTCCCTGG GCTCCATGAC	60
ACTGGCCTGG AGTGACTCAT TGCTCTGGTT GGTTGAGAGA GCTCCTTGC CAACAGGCCT	120
CCAAGTCAGG GCTGGGATTT GTTTCCTTTC CACATTCTAG CAACAATATG CTGGCCACTT	180
CCTGAACAGG GAGGGTGGGA GGAGCCAGCA TGGAAACAAGC TGCCACTTTC TAAAGTAGCC	240
AGACTTGCCC CTGGCCCTGT CACACCTACT GATGACCTTC TGTGCCTGCA GGATGGAATG	300
TAGGGGTGAG CTGTGTGACT CTATGGT	327

(2) INFORMATION FOR SEQ ID NO:147:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 173 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:147:

ACATTGTTTT TTTGAGATAA AGCATTGANA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTC AGTTCCATGT TTATAGCCTA GTT	173

(2) INFORMATION FOR SEQ ID NO:148:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 477 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:148:

ACAACCACCTT TATCTCATCG AATTTTTAAC CCAAACATCAC TCACTGTGCC TTTCTATCCT	60
ATGGGATATA TTATTTGATG CTCCATTCA TCACACATAT ATGAATAATA CACTCATACT	120
GCCCTACTAC CTGCTGCAAT AATCACATT CCTTCCTGTC CTGACCCCTGA AGCCATTGGG	180
GTGGTCCTAG TGGCCATCAG TCCANGCCTG CACCTTGAGC CCTTGAGCTC CATTGCTCAC	240
NCCANCCAC CTCACCGACC CCATCCTCTT ACACAGCTAC CTCCTTGCTC TCTAACCCCCA	300
TAGATTATNT CCAAATTCAAG TCAATTAAAGT TACTATTAAC ACTCTACCCG ACATGTCCAG	360
CACCACTGGT AAGCCTTCTC CAGCCAAACAC ACACACACAC ACACNCACAC ACACACATAT	420
CCAGGCACAG GCTACCTCAT CTTCACAAATC ACCCCTTAA TTACCATGCT ATGGTGG	477

(2) INFORMATION FOR SEQ ID NO:149:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 207 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:149:

ACAGTTGTAT TATAATATCA AGAAATAAAC TTGCAATGAG AGCATTAAAG AGGGAAGAAC	60
TAACGTATTT TAGAGAGCCA AGGAAGGTTT CTGTGGGGAG TGGGATGTAA GGTGGGGCCT	120

GATGATAAAAT AAGAGTCAGC CAGGTAAAGTG GGTGGTGTGG TATGGGCACA GTGAAGAAC	180
TTTCAGGCAG AGGGAACAGC AGTGAAA	207

(2) INFORMATION FOR SEQ ID NO:150:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 111 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:150:

ACCTTGATTT CATTGCTGCT CTGATGGAAA CCCAACTATC TAATTTAGCT AAAACATGGG	60
CACTTAAATG TGTCAGTGT TTGGACTTGT TAACTANTGG CATCTTGGG T	111

(2) INFORMATION FOR SEQ ID NO:151:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 196 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:151:

AGCGCGGCAG GTCATATTGA ACATTCCAGA TACCTATCAT TACTCGATGC TGTTGATAAC	60
AGCAAGATGG CTTTGAACTC AGGGTCACCA CCAGCTATTG GACCTTACTA TGAAAACCAT	120
GGATACCAAC CGGAAAACCC CTATCCCGCA CAGCCCCACTG TGGTCCCCAC TGTCTACGAG	180
GTGCATCCGG CTCAGT	196

(2) INFORMATION FOR SEQ ID NO:152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:152:

ACAGCACTTT CACATGTAAG AAGGGAGAAA TTCCTAAATG TAGGAGAAAG ATAACAGAAC	60
CTTCCCCTTT TCATCTAGTG GTGGAAACCT GATGCTTTAT GTTGACAGGA ATAGAACAG	120
GAGGGAGTTT GT	132

(2) INFORMATION FOR SEQ ID NO:153:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:153:

ACAAANACCCA NGANAGGCCA CTGGCCGTGG TGTCATGGCC TCCAAACATG AAAGTGTCA	60
CTTCTGCTCT TATGTCCTCA TCTGACAAC TCTTACCAT TTTATCCTCG CTCAGCAGGA	120
GCACATCAAT AAAGTCCAAA GTCTTGGACT TGGCCTTGGC TTGGAGGAAG TCATCAACAC	180
CCTGGCTAGT GAGGGTGC GGCGCTCCT GGATGACGGC ATCTGTGAAG TCGTGCACCA	240
GTCTGCAGGC CCTGTGGAAG CGCCGTCCAC ACGGAGTNAG GAATT	285

(2) INFORMATION FOR SEQ ID NO:154:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:154:

ACCACAGTCC TGTGAGGCCA GGGCTTCATG ACCCTTCTG TGAAAAGCCA TATTATCACC	60
ACCCCAAATT TTTCCTTAAA TATCTTAAC TGAAGGGGTC AGCCTCTTGA CTGCAAAGAC	120
CCTAACCGG TTACACAGCT AACTCCCCT GGCCTTGATT TGTGAAATTG CTGCTGCCTG	180
ATTGGCACAG GAGTCGAAGG TGTTCAGCT CCCTCCTCCG TGAACGAGA CTCTGATTG	240
AGTTTCACAA ATTCTCGGGC CACCTCGTCA TTGCTCCTCT GAAATAAAAT CCGGAGAATG	300
GTCAGGCTG TCTCATCCAT ATGGATCTTC CGG	333

(2) INFORMATION FOR SEQ ID NO:155:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 308 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:155:

ACTGGAAATA ATAAAACCCA CATCACAGTG TTGTGTCAA GATCATCAGG GCATGGATGG	60
GAAAGTGCCTT TGGGAACGTG AAAGTGCCTA ACACATGATC GATGATTTTT GTTATAATAT	120
TTGAATCACG GTGCATACAA ACTCTCCTGC CTGCTCCTCC TGGGCCCCAG CCCCAGCCCC	180
ATCACAGCTC ACTGCTCTGT TCATCCAGGC CCAGCATGTA GTGGCTGATT CTTCTTGGCT	240

GCTTTAGCC TCCANAAGTT TCTCTGAAGC CAACCAAACC TCTANGTGTA AGGCATGCTG	300
GCCCTGGT	308

(2) INFORMATION FOR SEQ ID NO:156:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 295 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:156:

ACCTTGCTCG GTGCTTGGAA CATATTAGGA ACTCAAAATA TGAGATGATA ACAGTGCCTA	60
TTATGATTA CTGAGAGAAC TGTTAGACAT TTACTGAAG ATTTCTACA CAGGAAGTGA	120
GAATAGGAGA TTATGTTGG CCCTCATATT CTCTCTATC CTCCCTGCTT CATTCTATGT	180
CTAATATATT CTCATCAAA TAAGGTTAGC ATAATCAGGA AATCGACCAA ATACCAATAT	240
AAAACCAGAT GTCTATCCTT AAGATTTCA AATAGAAAAC AAATTAACAG ACTAT	295

(2) INFORMATION FOR SEQ ID NO:157:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 126 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:157:

ACAAGTTAA ATAGTGTGT CACTGTGCAT GTGCTGAAAT GTGAAATCCA CCACATTTCT	60
GAAGAGCAAA ACAAAATTCTG TCATGTAATC TCTATCTTGG GTCGTGGGTA TATCTGTCCC	120
CTTAGT	126

(2) INFORMATION FOR SEQ ID NO:158:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 442 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:158:

ACCCACTGGT CTTGGAAACA CCCATCCTTA ATACGATGAT TTTCTGTGCG TGTGAAAATG	60
AANCCAGCAG GCTGCCCTA GTCACTCCTT CCTTCCAGAG AAAAAGAGAT TTGAGAAAAGT	120
GCCTGGGTAA TTCACCATTAA ATTCCTCCCC CCAAACCTCTC TGAGTCTTCC CTTAATATTT	180

CTGGTGGTTC TGACCAAAGC AGGTCATGGT TTGTTGAGCA TTTGGGATCC CAGTGAAGTA	240
NATGTTTGT A GCCTTGATA CTTAGCCCTT CCCACGCACA AACGGAGTGG CAGAGTGGTG	300
CCAACCCCTGT TTTCCCAGTC CACGTAGACA GATTCAAGT CGCGAATTCT GGAAGCTGGA	360
NACAGACGGG CTCTTGCAG AGCGGGACT CTGAGANGGA CATGAGGGCC TCTGCCTCTG	420
TGTTCATTC CTGATGTCT GT	442

(2) INFORMATION FOR SEQ ID NO:159:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 498 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:159:

ACTTCCAGGT AACGTTGTTG TTTCCGTTGA GCCTGAAC TG ATGGGTGACG TTGTAGGTTC	60
TCCAACAAGA ACTGAGGTTG CAGAGCGGGT AGGGAAGAGT GCTGTTCCAG TTGCACCTGG	120
GCTGCTGTGG ACTGTTGTTG ATTCCCTCACT ACGGCCCAAG GTTGTGGAAC TGGCANAAAG	180
GTGTGTTGTT GGANTTGAGC TCAGGGCGCT GTGGTAGGTT GTGGGCTCTT CAACAGGGC	240
TGCTGTGGTG CCGGGANGTG AANGTGTGTT GTCACTTGAG CTTGGCCAGC TCTGGAAAGT	300
ANTANATTCT TCCTGAAGGC CAGCGCTTGT GGAGCTGGCA NGGGTCANTG TTGTGTGTA	360
CGAACCCAGTG CTGCTGTGGG TGGGTGTANA TCCTCCACAA AGCCTGAAGT TATGGTGT	420
TCAGGTAANA ATGTGGTTTC AGTGTCCCTG GGCGNGCTGTG GAAGGTTGTA NATTGTCA	480
AAGGGAATAA GCTGTGGT	498

(2) INFORMATION FOR SEQ ID NO:160:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 380 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:160:

ACCTGCATCC AGCTTCCCTG CCAAACCTCAC AAGGAGACAT CAACCTCTAG ACAGGGAAAC	60
AGCTTCAGGA TACTTCCAGG AGACAGAGCC ACCAGCAGCA AAACAAATAT TCCCATGCCT	120
GGAGCATGGC ATAGAGGAAG CTGANAAATG TGGGGTCTGA GGAAGCCATT TGAGTCTGGC	180
CACTAGACAT CTCATCAGCC ACTTGTGTGA AGAGATGCC CATGACCCCCA GATGCCTCTC	240
CCACCCCTTAC CTCCATCTCA CACACTTGAG CTTTCCACTC TGTATAATTG TAACATCCTG	300
GAGAAAAATG CGAGTTTGAC CGAACCTGTT CACAACGGTA GAGGCTGATT TCTAACGAA	360
CTTGTAGAAT GAAGCCTGGA	380

(2) INFORMATION FOR SEQ ID NO:161:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 114 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:161:

ACTCCACATC CCCTCTGAGC AGGCGGTTGT CGTTCAAGGT GTATTTGGCC TTGCCTGTCA	60
CACTGTCCAC TGGCCCCTTA TCCACTTGGT GCTTAATCCC TCGAAAGAGC ATGT	114

(2) INFORMATION FOR SEQ ID NO:162:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 177 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:162:

ACTTTCTGAA TCGAATCAA TGATACTTAG TGTAGTTTA ATATCCTCAT ATATATCAA	60
GTTTACTAC TCTGATAATT TTGTAAACCA GGTAAACCAGA ACATCCAGTC ATACAGCTT	120
TGGTGATATA TAACTTGGCA ATAACCCAGT CTGGTGATAC ATAAAACATAC TCACTGT	177

(2) INFORMATION FOR SEQ ID NO:163:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 137 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:163:

CATTATACA GACAGGCCGT AAGACATTCA CGACAAAAAC GCGAAATTCT ATCCCGTGAC	60
CANAGAAGGC AGCTACGGCT ACTCCTACAT CCTGGCGTGG GTGGCCTTCG CCTGCACCTT	120
CATCAGCGGC ATGATGT	137

(2) INFORMATION FOR SEQ ID NO:164:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:164:

CTTATCACAA	TGAATGTTCT	CCTGGGCAGC	GTTGTGATCT	TTGCCACCTT	CGTGACTTTA	60
TGCAATGCAT	CATGCTATT	CATACTAAT	GAGGGAGTTC	CAGGAGATT	AACCAGGAAA	120
TGCATGGATC	TCAAAGGAAA	CAAACACCCA	ATAAACTCGG	AGTGGCAGAC	TGACAACGTG	180
GAGACATGCA	CTTGCTACGA	AACAGAAAATT	TCATGTTGCA	CCCTTGTTC	TACACCTGTG	240
GGTTATGACA	AAGACAAC	TCAAAGAAGG	AGGACTGCAA	GTATATCGTG	300	
GTGAGAAGA	AGGACCCAAA	AAAGACCTGT	TCTGTCAGTG	AATGGATAAT	CTAATGTGCT	360
TCTAGTAGGC	ACAGGGCTCC	CAGGCCAGGC	CTCATTCTCC	TCTGGCCTCT	AATAGTCAAT	420
GATTGTGTAG	CCATGCCTAT	CAGTAAAAG	ATNTTGAGC	AAACACTTT		469

(2) INFORMATION FOR SEQ ID NO:165:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 195 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:165:

ACAGTTTTT	ATANATATCG	ACATTGCCGG	CACTTGTGTT	CAGTTTCATA	AAGCTGGTGG	60
ATCCGCTGTC	ATCCACTATT	CCTGGCTAG	AGTAAAATT	ATTCTTATAG	CCCATGTCCC	120
TGCAGGCCGC	CCGCCCGTAG	TTCTCGTTCC	AGTCGTCTTG	GCACACAGGG	TGCCAGGACT	180
TCCTCTGAGA	TGAGT					195

(2) INFORMATION FOR SEQ ID NO:166:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (vi) ORIGINAL SOURCE:
- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:166:

ACATCTTAGT	AGTGTGGCAC	ATCAGGGGC	CATCAGGGTC	ACAGTCACTC	ATAGCCTCGC	60
CGAGGTCGGA	GTCCACACCA	CCGGTGTAGG	TGTGCTCAAT	CTTGGGCTTG	GCGCCACCT	120
TTGGAGAAGG	GATATGCTGC	ACACACATGT	CCACAAAGCC	TGTGAACCTG	CCAAAAGAATT	180
TTTGAGACCC	AGCCTGAGCA	AGGGCGGAT	GTTCAGCTTC	AGCTCCTCCT	TCGTCAGGTG	240
GATGCCAAC	TCGTCTANGG	TCCGTGGAA	GCTGGTGTCC	ACNTCACCTA	CAACCTGGGC	300
GANGATCTTA	TAAGAGGGCT	CCNAGATAAA	CTCCACGAAA	CTTCTCTGGG	AGCTGCTAGT	360
NGGGGCCTTT	TTGGTGAACT	TTC				383

(2) INFORMATION FOR SEQ ID NO:167:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 247 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:167:

ACAGAGCCAG ACCTTGGCCA TAAATGAANC AGAGATTAAG ACTAAACCCC AAGTCGANAT	60
TGGAGCAGAA ACTGGAGCAA GAAGTGGGCC TGGGGCTGAA GTAGAGACCA AGGCCACTGC	120
TATANCCATA CACAGAGCCA ACTCTCAGGC CAAGGCNATG GTTGGGGCAG ANCCAGAGAC	180
TCAATCTGAN TCCAAAGTGG TGGCTGGAAC ACTGGTCATG ACANAGGCAG TGACTCTGAC	240
TGANGTC	247

(2) INFORMATION FOR SEQ ID NO:168:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 273 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:168:

ACTTCTAAAGT TTCTAGAAG TGGAAGGATT GTANTCATCC TGAAAATGGG TTTACTTCAA	60
AATCCCTCAN CCTTGTTCTT CACNACTGTC TATACTGANA GTGTCATGTT TCCACAAAGG	120
GCTGACACCT GAGCCTGNAT TTTCACTCAT CCCTGAGAAG CCCTTTCCAG TAGGGTGGGC	180
AATTCCCCAAC TTCCTTGCCA CAAGCTTCCC AGGCTTTCTC CCCTGGAAAA CTCCAGCTTG	240
AGTCCCAGAT ACACTCATGG GCTGCCCTGG GCA	273

(2) INFORMATION FOR SEQ ID NO:169:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 431 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:169:

ACAGCCTTGG CTTCCCCAAA CTCCACAGTC TCAGTGCAGA AAGATCATCT TCCAGCAGTC	60
AGCTCAGACC AGGGTCAAAG GATGTGACAT CAACAGTTTC TGGTTTCAGA ACAGGTTCTA	120
CTACTGTCAA ATGACCCCCC ATACTTCCTC AAAGGCTGTG GTAAGTTTG CACAGGTGAG	180
GGCAGCAGAA AGGGGGTANT TACTGATGGA CACCATCTTC TCTGTATACT CCACACTGAC	240
CTTGGCATGG GCAAAGGCC C TACCACAAA ACAATAGGA TCACTGCTGG GCACCAGCTC	300
ACGCACATCA CTGACAACCG GGATGGAAAA AGAANTGCCA ACTTCATAC ATCCAACCTGG	360
AAAGTGATCT GATACTGGAT TCTTAATTAC CTTAAAAGC TTCTGGGGC CATCAGCTGC	420
TCGAACACTG .A	431

(2) INFORMATION FOR SEQ ID NO:170:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 266 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:170:

ACCTGTGGGC TGGGCTGTTA TGCCTGTGCC GGCTGCTGAA AGGGAGTTCA GAGGTGGAGC	60
TCAAGGAGCT CTGCAGGCAT TTTGCCAANC CTCTCCANAG CANAGGGAGC AACCTACACT	120
CCCCGCTAGA AAGACACCAAG ATTGGAGTCC TGGGAGGGGG AGTTGGGGTG GGCATTTGAT	180
GTATACTTGT CACCTGAATG AANGAGCCAG AGAGGAANGA GACGAANATG ANATTGGCCT	240
TCAAAGCTAG GGGTCTGGCA GGTGGA	266

(2) INFORMATION FOR SEQ ID NO:171:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1248 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:171:

GGCAGCCAAA TCATAAACCG CGAGGACTG CAGCCGCACT CGCAGCCCTG GCAGGGGGCA	60
CTGGTCATGG AAAACGAATT GTTCTGCTCG GGCCTCCTGG TGCACTCCGCA GTGGGTGCTG	120
TCAGCCGCAC ACTGTTCCA GAAGTGAGTG CAGAGCTCT ACACCACATCGG GCTGGGCCTG	180
CACAGCTTG AGGCCGACCA AGAGCCAGGG AGCCAGATGG TGGAGGCCAG CCTCTCCGTA	240
CGGCACCCAG AGTACAACAG ACCCTTGCTC GCTAACGACC TCATGCTCAT CAAGTTGGAC	300
GAATCCGTGT CGCAGTCTGA CACCATCCGG AGCATCAGCA TTGCTTCGCA GTGCCCTACC	360
GCGGGAACT CTTCGCTCGT TTCTGGCTGG GGTCTGCTGG CGAACGGCAG AATGCCCTACC	420
GTGCTGCAGT GCGTGAACGT GTCGGTGGTG TCTGAGGAGG TCTGCACTAA GCTCTATGAC	480
CCGCTGTACC ACCCCAGCAT GTTCTGCGCC GGCGGAGGGC AAGACCAGAA GGACTCCTGC	540
AACGGTGACT CTGGGGGGCC CCTGATCTGC AACGGGTACT TGCAAGGCCT TGTGTCTTTC	600
GGAAAAGCCC CGTGTGGCCA AGTTGGCGTG CCAGGTGTCT ACACCAACCT CTGCAAATTG	660
ACTGAGTGGG TAGAGAAAAC CGTCCAGGCC AGTTAACACT GGGGACTGGG AACCCATGAA	720
ATTGACCCCC AAATACATCC TGCAGGAAGGA ATTCAGGAAT ATCTGTTCCC AGCCCCCTCC	780
CCCTCAGGCC CAGGAGTCCA GGCCCCCAGC CCCTCTCTCC TCAAACCAAG GGTACAGATC	840
CCCAGCCCCC CCTCCCTCAG ACCCAGGAGT CCAGACCCCC CAGCCCCCTCC TCCCTCAGAC	900
CCAGGAGTCC AGCCCCCTCC CCCTCAGACCC CAGGAGTCCA GACCCCCCAG CCCCTCTCC	960
CTCAGACCCA GGGGTCCAGG CCCCCAACCC CTCCCTCCCT AGACTCAGAG GTCCAAGGCC	1020
CCAACCCNTC ATTCCCCAGA CCCAGAGGTC CAGGTCCAGG CCCCTCNTCC CTCAGACCCA	1080
GCGGTCCAAT GCCACCTAGA CTNTCCCTGT ACACAGTGCC CCCTTGTGGC ACGTTGACCC	1140
AACCTTACCA GTTGGTTTTT CATTNTNGT CCCTTCCCC TAGATCCAGA AATAAAAGTTT	1200
AAGAGAAGNG CAAAAAAA AAAAAAAA AAAAAAAA AAAAAAAA	1248

(2) INFORMATION FOR SEQ ID NO:172:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 159 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:172:

Met	Val	Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro
1					5									15	
Leu	Leu	Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser
	20					25								30	
Glu	Ser	Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr
	35				40							45			
Ala	Gly	Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Gly
	50				55							60			
Arg	Met	Pro	Thr	Val	Leu	Gln	Cys	Val	Asn	Val	Ser	Val	Val	Ser	Glu
	65				70				75				80		
Glu	Val	Cys	Ser	Lys	Leu	Tyr	Asp	Pro	Leu	Tyr	His	Pro	Ser	Met	Phe
	85					90						95			
Cys	Ala	Gly	Gly	Gly	Gln	Xaa	Gln	Xaa	Asp	Ser	Cys	Asn	Gly	Asp	Ser
	100					105						110			
Gly	Gly	Pro	Leu	Ile	Cys	Asn	Gly	Tyr	Leu	Gln	Gly	Leu	Val	Ser	Phe
	115				120							125			
Gly	Lys	Ala	Pro	Cys	Gly	Gln	Val	Gly	Val	Pro	Gly	Val	Tyr	Thr	Asn
	130				135							140			
Leu	Cys	Lys	Phe	Thr	Glu	Trp	Ile	Glu	Lys	Thr	Val	Gln	Ala	Ser	
	145				150							155			

(2) INFORMATION FOR SEQ ID NO:173:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1265 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:173:

GGCAGCCCGC	ACTCGCAGCC	CTGGCAGGCG	GCACTGGTCA	TGGAAAACGA	ATTGTTCTGC	60
TCGGCGTCC	TGGTGATCC	GCAGTGGGTG	CTGTCAGCCG	CACACTGTTT	CCAGAACTCC	120
TACACCATCG	GGCTGGGCCT	GCACAGTCTT	GAGGCCGACC	AAGAGCCAGG	GAGCCAGATG	180
GTGGAGGCCA	GCCTCTCCGT	ACGGCACCCA	GAGTACAACA	GACCCTTGCT	CGCTAACGAC	240

CTCATGCTCA TCAAGTTGGA CGAATCCGTG TCCGAGTCTG ACACCACCG GAGCAGTCAGC	300
ATTGCTTCGC AGTGCCTAC CGCGGGGAAC TCTTGCTCG TTTCTGGCTG GGGTCTGCTG	360
GCGAACGGTG AGCTCACGGG TGTGTCTCG CCCTCTTCAA GGAGGTCTC TGCCCAGTCG	420
CGGGGGCTGA CCCAGAGCTC TGCCTCCAG GCAGAATGCC TACCGTCTG CAGTGCCTGA	480
ACGTGTCGGT GGTGTCTGAG GAGGTCTGCA GTAAGCTCTA TGACCCGCTG TACCACCCCA	540
GCATGTTCTG CGCCGGCGA GGGCAAGACC AGAAGGACTC CTGCAACGGT GACTCTGGGG	600
GGCCCGTGAT CTGCAACGGG TACTTGCAAGG GCCTTGTGTC TTTCGAAAAA GCCCCGTGTG	660
GCCAAGTTGG CGTGCAGGT GTCTACACCA ACCTCTGCAA ATTCACTGAG TGGATAGAGA	720
AAACCGTCCA GCCCAGTTAA CTCTGGGGAC TGGGAACCCA TGAAATTGAC CCCCAAATAC	780
ATCCTGCGGA AGGAATTCAAG GAATATCTGT TCCCAGCCCC TCCTCCCTCA GGCCCAGGAG	840
TCCAGGCCCG CAGCCCTCC TCCCTCAAAC CAAGGGTACA GATCCCCAGC CCCTCCTCCC	900
TCAGACCCAG GAGTCCAGAC CCCCCAGCCC CTCCCTCCCTC AGACCCAGGA GTCCAGCCCC	960
TCCTCCNTCA GACCCAGGAG TCCAGACCCC CCAGCCCTC CTCCCTCAGA CCCAGGGTT	1020
GAGGCCCGCA ACCCCCTCTC CTTCAGAGTC AGAGGTCCAA GCCCCCAACCC CCTCGTTCCC	1080
CAGACCCAGA GTGNNAAGGTC CCAGCCCTC TTCCNTCAGA CCCAGNGGTC CAATGCCACC	1140
TAGATTTTCC CTGNACACAG TGCCCCCTTG TGGNANGTTG ACCAACCTT ACCAGTTGGT	1200
TTTCATTTT TNGTCCCTT CCCCTAGATC CAGAAATAAA GTTTAAGAGA NGNGCAAAAA	1260
AAAAAA	1265

(2) INFORMATION FOR SEQ ID NO:174:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1459 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:174:

GGTCAAGCCGC ACACGTTTTC CAGAAGTGAG TGCAGAGCTC CTACACCACATC GGGCTGGGCC	60
TGCACAGTCT TGAGGCCGAC CAAGAGCCAG GGAGCCAGAT GGTGGAGGCC AGCCTCTCCG	120
TACGGCACCC AGAGTACAAC AGACCCCTGC TCGCTAACGA CCTCATGCTC ATCAAGTTGG	180
ACGAATCCGT GTCCGAGTCT GACACCACCC GGAGCATCAG CATTGCTTCG CAGTGCCTA	240
CCGCGGGAA CTCTTGCTC GTTTCTGGCT GGGGCTGCT GCGAACGGT GAGCTCACGG	300
GTGTGTGCT GCCCTCTTCA AGGAGGTCTT CTGCCCCAGTC GCGGGGGCTG ACCCAGAGCT	360
CTGCGTCCCA GGCAGAATGC CTACCGTCT GCAGTGCCTG AACGTGTCGG TGGTGTCTGA	420
NGAGGTCTGC ANTAAGCTCT ATGACCCGCT GTACCAACCC ANCAGTGTCT GCGCCGGCGG	480
AGGCAAGAC CAGAAGGACT CCTGCAACGT GAGAGAGGG AAAGGGGAGG GCAGGGCAGT	540
CAGGGAAGGG TGGAGAAGGG GGAGACAGAG ACACACAGGG CGCGCATGGCG AGATGCAGAG	600
ATGGAGAGAC ACACAGGGAG ACAGTGACAA CTAGAGAGAG AAATGAGAG AAACAGAGAA	660
ATAAACACAG CAATAAGAG AAGCAAAGGA AGAGAAAGAAC AGAAACAGAC ATGGGGAGGC	720
AGAAACACAC ACACATAGAA ATGCAAGTGA CCTTCCAACA GCATGGGGCC TGAGGGCGGT	780
GACCTCCACC CAATAGAAAA TCCTCTTATA ACTTTTGACT CCCCAAAAAC CTGACTAGAA	840
ATAGCCTACT GTTGACGGGG AGCCTTACCA ATAACATAAA TAGTCGATTT ATGCATACGT	900
TTTATGCATT CATGATATAC CTTTGTGGA ATTTTTGAT ATTCTAAGC TACACAGTC	960
GTCTGTGAAT TTTTTAAAT TGTGCAACT CTCTTAAAT TTTTCTGATG TGTGTTATTGA	1020
AAAAATCCAA GTATAAGTGG ACTTGTGCAT TCAAACCCAGG GTTGTCAAG GGTCAACTGT	1080
GTACCCAGAG GGAAACAGTG ACACAGATTG ATAGAGGTGA AACACGAAGA GAAACAGGAA	1140
AAATCAAGAC TCTACAAAGA GGCTGGGCAG GGTGGCTCAT GCCTGTAATC CCAGCACTT	1200
GGGAGGCAGAG GCAGGGCAGAT CACTTGAGGT AAGGAGTCA AGACCCAGCCT GGCCAAAATG	1260
GTGAAATCCT GTCTGTACTA AAAATACAAA AGTTAGCTGG ATATGGTGGC AGGCGCTGT	1320
AATCCCAGCT ACTTGGGAGG CTGAGGCAGG AGAATTGCTT GAATATGGGA GGCAGAGGTT	1380
GAAGTGAGTT GAGATCACAC CACTATACTC CAGCTGGGC AACAGAGTAA GACTCTGTCT	1440
CAAAAAAAAAA AAAAAAAAAA	1459

(2) INFORMATION FOR SEQ ID NO:175:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:175:

GCGCAGCCCT	GGCAGGCGGC	ACTGGTCATG	GAAAACGAAT	TGTTCTGCTC	GGGCGTCCTG	60
GTGCATCCGC	AGTGGGTGCT	GTCAGCCGCA	CACTGTTCC	AGAACTCCTA	CACCATCGGG	120
CTGGCCCTGC	ACAGTCTTGA	GGCCGACCAA	GAGCCAGGGA	GCCAGATGGT	GGAGGCCAGC	180
CTCTCCGTAC	GGCACCCAGA	GTACAACAGA	CTCTTGCTCG	CTAACGACCT	CATGCTCATC	240
AAGTTGGACG	AATCCGTGTC	CGAGTCTGAC	ACCATCCGGA	GCATCAGCAT	TGCTTCGAG	300
TGCCCTACCG	CGGGGAACTC	TTGCCTCGTN	TCTGGCTGGG	GTCAGTCGAG	GAACGGCAGA	360
ATGCCTACCG	TGCTGCACTG	CGTGAACGTG	TCGGTGGTGT	CTGAGGANGT	CTGCAGTAAG	420
CTCTATGACC	CGCTGTACCA	CCCCAGCATG	TTCTGCGCCG	GCGGAGGGCA	AGACCAGAAG	480
GACTCCTGCA	ACGGTGAATC	TGGGGGGCCC	CTGATCTGCA	ACGGGTACTT	GCAGGGCCTT	540
GTGTCTTCG	GAAAAGCCCC	GTGTGGCCAA	CTTGGCGTGC	CAGGTGTCTA	CACCAACCTC	600
TGCAAATTCA	CTGAGTGGAT	AGAGAAAACC	GTCCAGNCCA	GTAACTCTG	GGGACTGGGA	660
ACCCATGAAA	TTGACCCCCA	AATACATCCT	GCGGAANGAA	TTCAAGGATA	TCTGTTCCCA	720
GCCCCCTCCTC	CCTCAGGCC	AGGAGTCCAG	GCCCCCAGCC	CCTCCTCCCT	CAAACCAAGG	780
GTACAGATCC	CCAGCCCCCTC	CTCCCTCAGA	CCCAAGGAGTC	CAGACCCCCC	AGCCCCCTCNT	840
CCNTCAGACC	CAGGAGTCCA	GCCCCCTCCTC	CNTCAGACGC	AGGAAGTCCAG	ACCCCCCAGC	900
CCNTCCTCCG	TCAGACCCAG	GGGTGCAGGC	CCCCAACCCC	TCTCCNTCA	GAGTCAGAGG	960
TCCAAGCCCC	CAACCCCTCG	TTCCCCAGAC	CCAGAGGTNC	AGGTCCCAGC	CCCTCCTCCC	1020
TCAGACCCAG	CGGTCCAATG	CCACCTAGAN	TNTCCCTGTA	CACAGTGC	CCTTGTGGCA	1080
NGTGACCCA	ACCTTACCAAG	TTGGTTTTTC	ATTTTTGTC	CCTTTCCCT	AGATCCAGAA	1140
ATAAAGTNTA	AGAGAAGCGC	AAAAAAA				1167

(2) INFORMATION FOR SEQ ID NO:176:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:176:

Met	Glu	Asn	Glu	Lle	Phe	Cys	Ser	Gly	Val	Lle	Val	His	Pro	Gln	Trp.
1															
					5						10				15

Val	Lle	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Lle
					20						25				30

Gly	Lle	His	Ser	Lle	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
					35				40			45			

Glu	Ala	Ser	Lle	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Lle	Lle	
					50				55			60			

Ala Asn Asp Leu Met Leu Ile Lys Leu Asp Glu Ser Val Ser Glu Ser
 65 70 75 80

 Asp Thr Ile Arg Ser Ile Ser Ile Ala Ser Gln Cys Pro Thr Ala Gly
 85 90 95

 Asn Ser Cys Leu Val Ser Gly Trp Gly Leu Leu Ala Asn Gly Arg Met
 100 105 110

 Pro Thr Val Leu His Cys Val Asn Val Ser Val Val Ser Glu Xaa Val
 115 120 125

 Cys Ser Lys Leu Tyr Asp Pro Leu Tyr His Pro Ser Met Phe Cys Ala
 130 135 140

 Gly Gly Gly Gln Asp Gln Lys Asp Ser Cys Asn Gly Asp Ser Gly Gly
 145 150 155 160

 Pro Leu Ile Cys Asn Gly Tyr Leu Gln Gly Leu Val Ser Phe Gly Lys
 165 170 175

 Ala Pro Cys Gly Gln Leu Gly Val Pro Gly Val Tyr Thr Asn Leu Cys
 180 185 190

 Lys Phe Thr Glu Trp Ile Glu Lys Thr Val Gln Xaa Ser
 195 200 205

(2) INFORMATION FOR SEQ ID NO:177:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1119 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:177:

GGCGACTCGC AGCCCTGGCA GGCGGCACGTG GTCATGGAAA ACGAATTGTT	60
GTCCTGGTGC ATCCGCAGTG GGTGCTGTCA GCCGCACACT GTTTCCAGAA	120
ATCGGGCTGG GCCTGCACAG TCTTGAGGCC GACCAAGAGC CAGGGAGCCA	180
GCCAGCCTCT CGGTACGGCA CCCAGAGTAC AACAGACCCCT TGCTCGCTAA	240
CTCATCAAGT TGGACGAATC CGTGTCCGAG TCTGACACCA TCCGGAGCAT	300
TCGCAGTGCC CTACCGCGGG GAACCTTGTG CTCGTTCTG GCTGGGGTCT	360
GATGCTGTGA TTGCCATCCA GTCCCAGACT GTGGGAGGCT GGGAGTGTGA	420
CAACCCCTGGC AGGGTTGTAC CATTTCGGCA ACTTCCAGTG CAAGGACGTC	480
CTCACTGGGT GCTCACTACT GCTCACTGCA TAACCCGGAA CACTGTGATC	540
CACCATAGTT CTCCGAAGTC AGACTATCAT GATTACTGTG TTGACTGTGC	600
ACTAACCATG CCGATGTTA GGTGAAATTA GCGTCACTTG GCCTCAACCA	660
CAGTTATCCT CACTGAATTG AGATTTCTG CTTCAGTGTG AGCCATTCCC	720
TGACCTACAG AGGTGAGGGA TCATATAAGCT CTTCAAGGAT GCTGGTACTC	780
TTCAATTCTC CTGTTGTAGT GAAAGGTGCG CCCTCTGGAG CCTCCCAGGG	840
GGTCACAATG ATGAATGTAT GATCGTGTTC CCATTACCCA AAGCCTTTAA	900
CTCAGTACAC CAGGGCAGGT CTAGCATTTC TTCATTAGT GTATGCTGTC	960
ACCACCTCAG GACTCCTGGA TTCTCTGCCT AGTTGAGCTC CTGCATGCTG	1020
GAGGTGAGGG AGAGGGCCCA TGGTTCAATG GGATCTGTGC AGTTGTAACA	1080

TTAATAAACAA GAAGCTGTGA TGTTAAAAAA AAAAAAAA

1119

(2) INFORMATION FOR SEQ ID NO:178:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 164 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:178:

Met	Glu	Asn	Glu	Leu	Phe	Cys	Ser	Gly	Val	Leu	Val	His	Pro	Gln	Trp
1				5					10				15		

Val	Leu	Ser	Ala	Ala	His	Cys	Phe	Gln	Asn	Ser	Tyr	Thr	Ile	Gly	Leu
	20						25					30			

Gly	Leu	His	Ser	Leu	Glu	Ala	Asp	Gln	Glu	Pro	Gly	Ser	Gln	Met	Val
	35				40					45					

Glu	Ala	Ser	Leu	Ser	Val	Arg	His	Pro	Glu	Tyr	Asn	Arg	Pro	Leu	Leu
	50				55				60						

Ala	Asn	Asp	Leu	Met	Leu	Ile	Lys	Leu	Asp	Glu	Ser	Val	Ser	Glu	Ser
	65				70			75				80			

Asp	Thr	Ile	Arg	Ser	Ile	Ser	Ile	Ala	Ser	Gln	Cys	Pro	Thr	Ala	Gly
	85				90					95					

Asn	Ser	Cys	Leu	Val	Ser	Gly	Trp	Gly	Leu	Leu	Ala	Asn	Asp	Ala	Val
			100				105				110				

Ile	Ala	Ile	Gln	Ser	Xaa	Thr	Val	Gly	Gly	Trp	Glu	Cys	Glu	Lys	Leu
			115				120			125					

Ser	Gln	Pro	Trp	Gln	Gly	Cys	Thr	Ile	Ser	Ala	Thr	Ser	Ser	Ala	Arg
	130				135					140					

Thr	Ser	Cys	Cys	Ile	Leu	Thr	Gly	Cys	Ser	Leu	Leu	Leu	Thr	Ala	Ser
145				150					155				160		

Pro Gly Thr Leu

(2) INFORMATION FOR SEQ ID NO:179:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:179:

CTGGAGTGCC TTGGTGTTC AAGCCCCTGC AGGAAGCAGA ATGCACCTTC TGAGGCACCT 60

CCAGGCTGCC	CCGGCCGGGG	GATGCGAGGC	TGGGAGCACC	CTTGGCCCGGC	TGTGATTGCT	120
GCCAGGCAC	GTTCATCTCA	GCTTTCTGT	CCCTTGCTC	CCGGCAAGCG	CTTCTGCTGA	180
AAGTTCATAT	CTGGAGCCTG	ATGTCTAAC	GAATAAAGGT	CCCATGCTCC	ACCCGAAAAAA	240
AAAAAAAAAA						250

(2) INFORMATION FOR SEQ ID NO:180:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 202 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:180:

ACTAGTCCAG	TGTGGTGGAA	TTCCATTGTG	TTGGGCCCAA	CACAATGGCT	ACCTTTAACAA	60
TCACCCAGAC	CCCGCCCCCTG	CCCGTGGCCC	ACGCTGCTGC	TAACGACAGT	ATGATGCTTA	120
CTCTGCTACT	CGGAAACTAT	TTTTATGTAA	TTAATGTATG	CTTTCTTGTT	TATAATGCC	180
TGATTAAAAA	AAAAAAAAAA					202

(2) INFORMATION FOR SEQ ID NO:181:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 558 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:181:

TCCYTTTGKT	NAGGTTTKKG	AGACAMCCCK	AGACCTWAAN	CTGTGTCACA	GACTTCYNGG	60
AATGTTTAGG	CAGTGCTAGT	AATTCYTCG	TAATGATTCT	GTTTATTACTT	TCCTNATTCT	120
TTATTCCTCT	TTCTTCTGAA	GATTAATGAA	GTTGAAAATT	GAGGTGGATA	AATACAAAAAA	180
GGTAGTGTGA	TAGTATAAGT	ATCTAAGTCC	AGATGAAAGT	GTGTTATATA	TATCCATTCA	240
AAATTATGCA	AGTTAGTAAT	TACTCAGGGT	TAACTAAATT	ACTTTAATAT	GCTGTTGAAC	300
CTACTCTGTT	CCTGGCTAG	AAAAAATTAT	AAACAGGACT	TTGTTAGTTT	GGGAAGCCAA	360
ATTGATAATA	TTCTATGTT	TAAAAGTTGG	GCTATACATA	AATTATTAAG	AAATATGGAW	420
TTTTATTCCC	AGGAATATGG	KGTTCACTTT	ATGAATATTA	CSCRGGATAG	AWGTWTGAGT	480
AAAAYCAGTT	TTGGTWAATA	YGTWAATATG	TCMTAAATAA	ACAAGKCTTT	GACTTATTTC	540
CAAAAAAAAAA	AAAAAAAAAA					558

(2) INFORMATION FOR SEQ ID NO:182:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 479 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:182:

ACAGGGWTTK	GRGGATGCTA	AGSCCCCCRGA	RWTYGTTGA	TCCAACCTG	GCTTWTTTTTC	60
AGAGGGAAA	ATGGGGCCTA	GAAGTTACAG	MSCATYTAGY	TGGTGCGMTG	GCACCCCTGG	120
CSTCACACAG	ASTCCCGAGT	AGCTGGGACT	ACAGGCACAC	AGTCACTGAA	GCAGGCCCCCTG	180
TTWGCAATT	ACGTTGCCAC	CTCCAACTTA	AAACATTCTTC	ATATGTGATG	TCCTTAGTCA	240
CTAAGGTTAA	ACTTTCCAC	CCAGAAAAGG	CAACTTAGAT	AAAATCTTAG	AGTACTTTCA	300
TACTMMTCTA	AGTCCTCTTC	CAGCCTCACT	KKGAGTCCM	CYTGGGGTT	GATAGGAANT	360
NTCTCTTGGC	TTTCTCAATA	AARTCTCATAT	YCATCTCATG	TTAATTTGG	TACGCATARA	420

AWTGSTGARA AAATTAAAAAT GTTCTGGTTY MACTTTAAAA ARAAAAAAAA AAAAAAAA 479

(2) INFORMATION FOR SEQ ID NO:183:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:183:

AGGCAGGGAGC AGAACGCTAAA	GCCAAAGGCC	AAGAACAGTG	GCAGTGCCAG	CACTGGTGCC	60
AGTACCAAGTA CCAATAACAG	TGCCAGTGCC	AGTGCAGCA	CCAGTGGTGG	CTTCAGTGCT	120
GGTCCCAGCC TGACCGCCAC	TCTCACATTT	GGGACTCTTCG	CTGGCCTTGG	TGGAGCTGGT	180
GCCAGCACCA GTGGCAGCTC	TGGTGCCTGT	GGTTTCTCCT	ACAAGTGAGA	TTTTAGATAT	240
TGTTAACCTCT GGCAGTCTTT	CTCTTCAGC	CAGGGTGCAT	CCTCAGAAC	CTACTCAACA	300
CAGCACTCTA GGCAAGCCACT	ATCAATCAAT	TGAAGTTGAC	ACTCTGCATT	ARATCTATT	360
GCCATTCAA AAAAAAAA	AAAAAA				384

(2) INFORMATION FOR SEQ ID NO:184:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 496 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:184:

ACCGAATTGG GACCGCTGGC	TTATAAGCGA	TCATGTYNT	CCRGTATKAC	CTCAACGAGC	60
AGGGAGATCG AGTCTATACG	CTGAAGAAAT	TTGACCCGAT	GGGACAAACAG	ACCTGCTCAG	120
CCCATCCTGC TCGGTTCTCC	CCAGATGACA	AATACTCTSG	ACACCGAAC	ACCATCAAGA	180
AACGCTTCAA GGTGCTCATG	ACCCAGCAAC	CGCCCCCTGT	CCTCTGAGGG	TCCCTTAAAC	240
TGATGTCTTT TCTGCCACCT	GTTACCCCTC	GGAGACTCCG	TAACCAAAC	CTTCGGACTG	300
TGAGCCCTGA TGCCTTTTG	CCAGCCATAC	TCTTGGCAT	CCAGTCTCTC	GTGGCGATTG	360
ATTATGCTTG TGTGAGGCAA	TCATGGTGGC	ATCACCCATA	AAGGGAACAC	ATTTGACTTT	420
TTTTCTCAT ATTTAAATT	ACTACMAGAW	TATTW MAGAW	WAAATGA WTT	GAAAAACTST	480
AAAAAAAAAA	AAAAAA				496

(2) INFORMATION FOR SEQ ID NO:185:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 384 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:185:

GCTGGTAGCC TATGGCGKGG	CCCACGGAGG	GGCTCCTGAG	GCCACGGRAC	AGTGACTTCC	60
CAAGTATCYT GCGCSGCGTC	TTCTACCGTC	CCTACCTGCA	GATCTTCGGG	CAGATTCCCC	120
AGGAGGACAT GGACGTGGCC	CTCATGGAGC	ACAGCAACTG	YTCGTCGGAG	CCCGGCTTCT	180
GGGCACACCC TCCTGGGGCC	CAGGCAGGCA	CCTGCGTCTC	CCAGTATGCC	AACTGGCTGG	240
TGGTGTGCT CCTCGTCATC	TTCTGCTCG	TGGCCAACAT	CCTGCTGGTC	AACTTGCTCA	300
TTGCCATGTT CAGTTACACA	TTCGGCAAAG	TACAGGGCAA	CAGCGATCTC	TACTGGGAAG	360
GCGCAGCGTT ACCGCCTCAT	CCGG				384

(2) INFORMATION FOR SEQ ID NO:186:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 577 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:186:

GAGTTAGCTC	CTCCACAACC	TTGATGAGGT	CGTCTGCAGT	GGCCTCTCGC	TTCATACCGC	60
TNCCATCGTC	ATACTGTAGG	TTTGCCACCA	CYTCCCTGGCA	TCTTGGGGCG	GCNTAATATT	120
CCAGGAAACT	CTCAATCAAG	TCACCGTCGA	TGAAACCTGT	GGGCTGGTTC	TGTCTTCGC	180
TCGGTGTGAA	AGGATCTCCC	AGAAGGGAGTG	CTCGATCTTC	CCCACACTTT	TGATGACTTT	240
ATTGAGTCGA	TTCTGCATGT	CCAGCAGGAG	GTGTACCCAG	CTCTCTGACA	GTGAGGTAC	300
CAGCCCTATC	ATGCCGTTGA	MCGTCCGAA	GARCACCGAG	CCTTGTGTGG	GGGKKGAAGT	360
CTCACCCAGA	TTCTGCATTA	CCAGAGAGCC	GTGGCAAAG	ACATTGACAA	ACTCGCCCCAG	420
GTGGAAAAAG	AMCAMCTCCT	GGARGTGTCTN	GCCGCTCCTC	GTCMGTGGT	GGCAGCGCTW	480
TCCTTTGAC	ACACAAACAA	GTAAAGGCA	TTTCAAGCCC	CCAGAAAANTT	GTCATCATCC	540
AAGATNTCGC	ACAGCACTNA	TCCAGTTGGG	ATTAAT			577

(2) INFORMATION FOR SEQ ID NO:187:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 534 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:187:

AACATCTTCC	TGTATAATGC	TGTGTAATAT	CGATCCGATN	TTGTCTGSTG	AGAATYCATW	60
ACTKGAAAAA	GMAACATTA	AGCCTGGACA	CTGGTATTAA	AATTACAAT	ATGCAACACT	120
TTAAACAGTG	TGTCATCTG	CTCCCYNNAC	TTTGTATCA	CCAGTCTGGG	AAKAAGGGTA	180
TGCCCTATT	ACACCTGTTA	AAAGGGCGCT	AAGCATTTTT	GATTCAACAT	CTTTTTTTT	240
GACACAAGTC	CGAAAAAAAGC	AAAAGTAAAC	AGTTATYAT	TTGTTAGCCA	ATTCACTTTC	300
TTCATGGGAC	AGAGCCATYT	GATTTAAAAA	GCAAATTGCA	TAATATTGAG	CTTYGGGAGC	360
TGATATTTGA	GCGGAAGAGT	AGCCTTCTA	CTTCACCAGA	CACAACCTCC	TTTCATATTG	420
GGATGTTNAC	NAAAGTWATG	TCTCTWACAG	ATGGGATGCT	TTTGTGGCAA	TTCTGTTCTG	480
AGGATCTCCC	AGTTTATT	CCACTTGCAC	AAGAAGGCGT	TTCTTCCTC	AGGC	534

(2) INFORMATION FOR SEQ ID NO:188:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 761 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:188:

AGAAAACCAGT	ATCTCTAAA	ACAACCTCTC	ATACCTTG	GACCTAATT	TGTGTGCGTG	60
TGTGTGTGCG	CGCATATTAT	ATAGACAGGC	ACATCTTTT	TACTTTGTA	AAAGCTTATG	120
CCTCTTTGGT	ATCTATATCT	GTGAAAGTT	TAATGATCTG	CCATAATGTC	TTGGGGACCT	180
TTGTCTTCTG	TGTAAATGGT	ACTAGAGAAA	ACACCTATNT	TATGAGTCAA	TCTAGTTNGT	240
TTTATTCGAC	ATGAAGGAAA	TTTCCAGATN	ACAACACTNA	CAAACCTCTCC	CTKGACKARG	300
GGGGACAAAG	AAAAGCAAAA	CTGAMCATAA	RAAACAAATWA	CCTGGTGAGA	ARTTGCAAA	360
ACAGAAATWR	CGTAGTATAT	TGAARNACAG	CATCATTAAA	RMGTTWTKT	WTCTCCCTT	420

GCAAAAAACA	TGTACNGACT	TCCC GTTGAG	TAATGCCAAG	TTGTTTTTTT	TATNATAAAA	480
CTTGCCTTC	ATTACATGTT	TNAAAGTGGT	GTGGTGGGCC	AAAATATTGA	AATGATGGAA	540
CTGACTGATA	AAGCTGTACA	AATAAGCAGT	GTGCC TAACA	AGCAACACAG	TAATGTTGAC	600
ATGCTTAATT	CACAAATGCT	AATTCTATTA	TAATGTTTG	CTAAAATACA	CTTTGAACTA	660
TTTTCTGTN	TTCCCAGAGC	TGAGATNTTA	GATTTATGT	AGTATNAAGT	AAAAAANTAC	720
GAAAAATAATA	ACATTGAAGA	AAAANANAAA	AAANAAAAAA	A		761

(2) INFORMATION FOR SEQ ID NO:189:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:189:

TTTTTTTTT	TTTGCCGATN	CTACTATTTT	ATTGCAGGAN	GTGGGGGTGT	ATGCACCGCA	60
CACC GGGGCT	ATNAGAAGCA	AGAAGGAAGG	AGGGAGGGCA	CAGCCCCTTG	CTGAGCAACA	120
AAGCCGCTG	CTGCC TCTC	TGTC TGTCTC	CTGGTGCAGG	CACATGGGGA	GACCTTCCCC	180
AAGGCAGGGG	CCACCA GTCC	AGGGGTGGGA	ATACAGGGGG	TGGGANGTGT	GCATAAGAAG	240
TGATAGGCAC	AGGCCACCCG	GTACAGACCC	CTCGGCTCT	GACAGGTNGA	TTTCGACCAG	300
GTCATTGTGC	CCTGCC CAGG	CACAGCGTAN	ATCTGGAAAA	GACAGAATGC	TTTCCTTTTC	360
AAATTG GCT	NGTCATNGAA	NGGC CANTTT	TCCA ANTTNG	GCTNGGTCTT	GGTACNCTTG	420
GTTCGGCCCA	GCTCCNCGTC	CAAA AANTAT	TCACCCNNCT	CCNAATTGCT	TGCNGGNCCC	480
CC						482

(2) INFORMATION FOR SEQ ID NO:190:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 471 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:190:

TTTTTTTTT	TTTAAACACA	ACAAAATTAA	TTAGAAGAAT	AGTGGTTTG	60
AAAAC TCTCG	CATCCAGTGA	GAACT ACCAT	ACACCACATT	ACAGCTNGGA	120
AATGTCTGGT	CAAATGATAC	AATGGAACCA	TTCAATCTTA	CACATGCACG	180
CGCTTTGAC	ATACAATGCA	CAAAAAAAA	AGGGGGGGGG	GACCACATGG	240
TAAGTACTCA	TCACATACAT	TAAGACACAG	TTCTAGTCCA	GTCNAAAATC	300
TGAAAATTT	CATGTATGCA	ATCCAACAA	AGAACTTNAT	TGGT GATCAT	360
CTACATCNAC	CTTGATCATT	GCCAGGAACN	AAAAGTTNAA	ANCACNCNGT	420
TCTGTAATTN	ANTTCAACCT	CCGTACNGAA	AAATTTNNNT	TATACACTCC	471
C					

(2) INFORMATION FOR SEQ ID NO:191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:191:

GAGGGATTGA	AGGTCTGTTC	TASTGTCGGM	CTGTT CAGCC	ACCAACTCTA	ACAAGTTGCT	60
GTCTTCCACT	CACTGTCTGT	AAGCTTTTA	ACCCAGACWG	TATCTCATA	AATAGAACAA	120

ATTCCTTCACC AGTCACATCT TCTAGGACCT TTTGGATTG AGTTAGTATA AGCTCTCCA	180
CTTCCTTGT TAAGACTTCA TCTGGTAAAG TCTTAAGTT TGAGAAAGG AATTYAATTG	240
CTCGTTCTCT AACAAATGTCC TCTCCTTGAA GTATTTGGCT GAACAACCCA CCTAAAGTCC	300
CTTGTCAT CCATTTAAA TATACTTAAT AGGGCATTGK TNCACTAGGT TAAATTCTGC	360
AAGAGTCATC TGTCTGAAA AGTTGCGTTA GTATATCTGC CA	402

(2) INFORMATION FOR SEQ ID NO:192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 601 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:192:

GAGCTGGAT CCAATAATCT TTGTCAGGAG GCAGCACACA TATNCAGTGC CATGGNAACT	60
GGTCTACCCC ACATGGGAGC AGCATGCCGT AGNTATATAA GGTCATTCCC TGAGTCAGAC	120
ATGCYTYTTT GAYTACCGT TGCCAAGTGC TGGTGAATTCT YAACACACYT CCATCCCGYT	180
CTTTTGTTGA AAAACTGGCA CTTKTCTGAA ACTAGCARGA CATCACTTAC AAATTCAACCC	240
ACGAGACACT TGAAAGGTGT AACAAAGCGA YTCTTGCATT GCTTTTGTC CCTCCGGCAC	300
CAGTTGTCAA TACTAACCCG CTGGTTTGCC TCCATCACAT TTGTGATCTG TAGCTCTGGA	360
TACATCTCCT GACAGTACTG AAGAACTTCT TCTTTGTTT CAAAAGCARC TCTTGGTGCC	420
TGTTGGATCA GGTTCCATT TCCCAGTCYG AATGTTACAA TGCCATATT WACTTCCCAC	480
AAAACATTGC GATTGAGGC TCAGCAACAG CAAATCCTGT TCCGGCATTG GCTGCAAGAG	540
CCTCGATGTA GCCGGCCAGC GCCAAGGCAG GCGCCGTGAG CCCCACAGC AGCAGAAGCA	600
G	601

(2) INFORMATION FOR SEQ ID NO:193:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 608 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:193:

ATACAGCCCCA NATCCCACCA CGAAGATGCG CTTGTTGACT GAGAACCTGA TGCAGTCAGT	60
GGTCCCGCTG TAGCCCCAGC GACTCTCCAC CTGCTGGAG CGGTTGATGC TGCACTCYTT	120
CCCAACCGAG GCAGMAGCGG GSCCGGTCAA TGAACCTCCAY TCGTGGCTTG GGGTKGACGG	180
TKAAGTGCAG GAAGAGGGCTG ACCACCTCGC GGTCCACCGAG GATGCCCGAC TGTGCGGGAC	240
CTGCAGCGAA ACTCCTCGAT GGTCATGAGC GGGAAAGCGAA TGAGGCCCCAG GGCCTTGCCC	300
AGAACCTTCTC GCCTGTTCTC TGGCGTCAAC TGCAGCTGCT GCCGCTGACA CTCGGCCTCG	360
GACCAAGCGGA CAAACGGCRT TGAACAGCCG CACCTCACGG ATGCCCACTG TGTCGCGCTC	420
CAGGAMMGSC ACCAGCGTGT CCAGGTCAAT GTCGGTGAAG CCCTCCGCGG GTRATGGCGT	480
CTGCAGTGTGTT TTTGTCGATG TTCTCCAGGC ACAGGCTGGC CAGCTGCGGT TCATCGAAGA	540
GTCGCGCTG CGTGAGCAGC ATGAAGGCAGT TGTGGCTCG CAGTTCTTCT TCAGGAACTC	600
CACGCAAT	608

(2) INFORMATION FOR SEQ ID NO:194:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:194:

GAACGGCTGG	ACCTTGCCTC	GCATTGTCGT	TGCTGGCAGG	GAATACCTTG	GCAAGCAGYT	60
CCAGTCGAG	CAGCCCCAGA	CCGCTGCCGC	CCGAAGCTAA	GCCTGCCTCT	GGCCTTCCCC	120
TCCGCCTCAA	TGCAGAACCA	GTAGTGGGAG	CACTGTGTTT	AGAGTTAAGA	GTGAACACTG	180
TTTGATTTA	CTTGGGAATT	TCCTCTGTTA	TATAGCTTTT	CCCAATGCTA	ATTTCCAAC	240
AACAACAACA	AAATAAACATG	TTTGCCTGTT	AAGTTGTATA	AAAGTAGGTG	ATTCTGTATT	300
TAAAGAAAAT	ATTACTGTTA	CATATACTGC	TTGCAATTTC	TGTATTTATT	GKTNCTSTGG	360
AAATAAATAT	AGTTATTAAA	GGTTGTCANT	CC			392

(2) INFORMATION FOR SEQ ID NO:195:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 502 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:195:

CCSTTKGAGG	GGTKAGGKYC	CAGTTYCCGA	GTGGAAGAAA	CAGGCCAGGA	GAAGTGCCTG	60
CCGAGCTGAG	GCAGATGTT	CCACAGTGAC	CCCCAGAGCC	STGGGSTATA	GTYTCTGACC	120
CCTCNCAAGG	AAAGACCACS	TTCTGGGAC	ATGGGCTGGA	GGGCAGGACC	TAGAGGCACC	180
AAGGGAAGGC	CCCATTCCCG	GGSTGTTCCC	CGAGGAGGAA	GGGAAGGGGC	TCTGTGTGCC	240
CCCCASGAGG	AAGAGGCCCT	GAGTCCTGGG	ATCAGACACC	CCTTCACGTG	TATCCCCACA	300
CAAATGCAAG	CTCACCAAGG	TCCCCTCTCA	GTCCCCTTCC	STACACCCCTG	AMCGCCACT	360
GSCSCACACC	CACCCAGAGC	ACGCCACCCG	CCATGGGAR	TGTGCTCAAG	GARTCGCNNG	420
GCARCGTGA	CATCTNGTCC	CAGAAGGGGG	CAGAATCTCC	AATAGANGGA	CTGARCMSTT	480
GCTNANAAAA	AAAAANAAAA	AA				502

(2) INFORMATION FOR SEQ ID NO:196:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 665 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:196:

GGTTACTTGG	TTTCATTGCC	ACCACTTAGT	GGATGTCATT	TAGAACCATT	TTGTCTGCTC	60
CCTCTGGAAG	CCTTGCGCAG	AGCGGACTTT	GTAATTGTTG	GAGAATAACT	GCTGAATT	120
WAGCTGTTK	GAGTTGATTG	GCACCACTGC	ACCCACAAC	TCAATATGAA	AACYAWTTGA	180
ACTWATTAT	TATCTTGTGA	AAAGTATAAC	AATGAAAATT	TTGTTCATAC	TGTATTKATC	240
AAGTATGATG	AAAAGCAAWA	GATATATATT	CTTTTATTAT	GTTAAATTAT	GATTGCCATT	300
ATTAATCGGC	AAAATGTGGA	GTGTATGTT	TTTCACAGT	AATATATGCC	TTTTGTAAC	360
TCACATTGGTT	ATTTTATTGT	AAATGARTTA	CAAATTCCTT	AATTAAAGAR	AATGGTATGT	420
WATATTTATT	TCATTAATT	CTTTCCTKGT	TTACGTWAAT	TTGAAAAGA	WTGCATGATT	480
TCTTGACAGA	AATCGATCTT	GATGCTGTTG	AAGTAGTTG	ACCCACATCC	CTATGAGTTT	540
TTCTTAGAAT	GTATAAAGGT	TGTAGCCCAT	CNAACCTCAA	AGAAAAAAAT	GACCACATAC	600
TTTGCATCA	GGCTGAAATG	TGGCATGCTN	TTCTAATTCC	AACTTTATAA	ACTAGCAAAN	660
	AAGTG					665

(2) INFORMATION FOR SEQ ID NO:197:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:197:

TTTNTTTTT	TTTTTTTG	AGGAAGGATT	CCATTTATTG	TGGATGCATT	TTCACAATAT	60
ATGTTTATTG	GAGCGATCCA	TTATCAGTGA	AAAGTATCAA	GTGTTATAA	NATTTTAGG	120
AAGGCAGATT	CACAGAACAT	GCTNGTCNGC	TTGCAGTTTT	ACCTCGTANA	GATNACAGAG	180
AATTATAGTC	NAACCAGTAA	ACNAGGAATT	TACTTTCAA	AAGATTAAT	CCAAACTGAA	240
CAAAATTCTA	CCCTGAAACT	TACTCCATCC	AAATATTGGA	ATAANAGTCA	GCAGTGATAC	300
ATTCTCTCT	GAACTTAGA	TTTCTAGAA	AAATATGAA	TAGTGATCG	GAAGAGCTCT	360
TGTTCAAAAG	TACAACNAAG	CAATGTC	TTACCATAGG	CCTTAATTCA	AACTTTGATC	420
CATTTCACTC	CCATCACGGG	AGTCAATGCT	ACCTGGGACA	CTTGTATTT	GTTCATNCTG	480
ANCNTGGCTT	AA					492

(2) INFORMATION FOR SEQ ID NO:198:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 478 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:198:

TTTNTTTGN	ATTCANTCT	GTANNAANTA	TTTCATTAT	GTTTATTANA	AAAATATNAA	60
TGTNTCCACN	ACAAATCATN	TTACNTNAGT	AAAGGCCAN	CTACATTGTA	CAACATACAC	120
TGAGTATATT	TTGAAAAGGA	CAAGTTAAA	GTANACNCAT	ATTGCCGANC	ATANCACATT	180
TATACATGGC	TTGATTGATA	TTTACGACAG	CANAAACTGA	GTGAGTTACC	AGAAANAAAT	240
NATATATGTC	AATCNGATTT	AAGATACAAA	ACAGATCCTA	TGGTACATAN	CATCNTGTAG	300
GAGTTGTGGC	TTTATGTTA	CTGAAAGTCA	ATGCAGTTCC	TGTACAAAGA	GATGGCCGTA	360
AGCATTCTAG	TACCTCTACT	CCATGGTTAA	GAATCGTACA	CTTATGTTA	CATATGTNCA	420
GGGTAAGAAT	TGTGTTAAGT	NAANTTATGG	AGAGGTCCAN	GAGAAAATT	TGATNCAA	478

(2) INFORMATION FOR SEQ ID NO:199:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 482 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:199:

AGTGACTTGT	CCTCCAACAA	AACCCCTG	TCAAGTTGT	GGCACTGACA	ATCAGACCTA	60
TGCTAGTTCC	TGTCATCTAT	TCGCTACTAA	ATGCAGACTG	GAGGGGACCA	AAAAGGGGCA	120
TCAACTCCAG	CTGGATTATT	TTGGAGCCTG	CAAATCTATT	CCTACTTGT	CGGACTTTGA	180
AGTGATTTCAG	TTTCCTCTAC	GGATGAGAGA	CTGGCTCAAG	AATATCCTCA	TGCAGCTTTA	240
TGAAGCCNAC	TCTGAACACG	CTGGTTATCT	NAGATGAGAA	NCAGAGAAAT	AAAGTCNAGA	300
AAATTTACCT	GGANGAAAAG	AGGCTTTNGG	CTGGGGACCA	TCCCATTGAA	CCTCTCTTA	360
ANGGACTTTA	AGAANAAACT	ACCACATGT	TGTGNTATCC	TGGTGCCNGG	CCGTTTANTG	420
AACNTNGACN	NCACCCNTNT	GGAATANANT	CTTGACNGCN	TCCTGAACCT	GCTCCTCTGC	480
GA						482

(2) INFORMATION FOR SEQ ID NO:200:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 base pairs
- (B) TYPE: nucleic acid

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:200:

CGGCCGCAAG TCGAACTCCA GCTGGGGCCG TGCGGACGAA GATTCTGCCA GCAGTTGGTC	60
CGACTGCGAC GACGGCGGC GCGACAGTCG CAGGTGCAGC CGGGCGCCCT GGGGTCTTGC	120
AAGGCTGAGC TGACGCCGA GAGGTCTGTGT CACGTCCCAC GACCTTGACG CCGTCGGGAA	180
CAGCCGGAAC AGAGCCCGGT GAANGCGGGA GGCTCGGGG AGCCCCTCGG GAAGGGCGGC	240
CCGAGAGATA CGCAGGTGCA GGTGGCCGCC	270

(2) INFORMATION FOR SEQ ID NO:201:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 419 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:201:

TTTTTTTTTT TTTTGGAAATC TACTGCGAGC ACAGCAGGTC AGCAACAAGT TTATTTGCA	60
GCTAGCAAGG TAACAGGGTA GGGCATGGTT ACATGTTCA GTCACATTCC TTTGTCTGG	120
TTGATTGGTT TGTCTTTATG GGGGCGGGGT GGGGTAGGGG AAANCGAACG ANAANTAAACA	180
TGGAGTGGGT GCACCCCTCCC TGTAGAACCT GGTTACNAAA GCTTGGGCA GTTCACCTGG	240
TCTGTGACCG TCATTTCTT GACATCAATG TTATTAGAAG TCAGGATATC TTTTAGAGAG	300
TCCACTGTNT CTGGAGGGAG ATTAGGGTTT CTTGCCAANA TCCAANCAA ATCCACNTGA	360
AAAAGTTGGA TGATNCANGT ACNGAATACC GANGGCATAN TTCTCATANT CGGTGGCCA	419

(2) INFORMATION FOR SEQ ID NO:202:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 509 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:202:

TTTNTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT TTTTTTTTTT	60
TGGCACTTAA TCCATTTTA TTTCAAAATG TCTACAAANT TTNAATNCNC CATTATAACNG	120
GTNATTTTNC AAAATCTAAA NNNTTATTCAA ATTNAGCCA AANTCCTTAC NCAAAATNNAA	180
TACNCNCAAA AATCAAAAAT ATACNTNTCT TTCAGCAAAC TTNGTTACAT AAATTAAAAA	240
AATATATACG GCTGGTGTTC TCAAAGTACA ATTATCTAA CACTGCAAAC ATNTTTNNAA	300
GGAACTAAAA TAAAAAAAAA CACTNCCGCA AAGGTTAAAG GGAACAACAA ATTCTNTTTA	360
CAACANCNNC NATTAAAAA ATCATATCTC AAATCTTAGG GGAATATATA CTTCACACNG	420
GGATCTTAAC TTTTACTNCA CTTTGTATTAT TTTTTANAA CCATTGTNTT GGGCCCAACA	480
CAATGGNAAT NCCNCCNCC TGGAAGTAGT	509

(2) INFORMATION FOR SEQ ID NO:203:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 583 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:203:

TTTTTTTTTT	TTTTTTTGA	CCCCCCTCTT	ATAAAAAAACA	AGTTACCATT	TTATTTTACT	60
TACACATATT	TATTTTATAA	TTGGTATTAG	ATATTCAAAA	GGCAGCTTTT	AAAATCAAAC	120
TAATGGAAA	CTGCCTTAGA	TACATAATTC	TTAGGAATTA	GCTTAAAATC	TGCCTAAAGT	180
GAAAATCTTC	TCTAGCTCTT	TTGACTGTAA	ATTTTGACT	CTTGAAAAC	ATCCAAATT	240
ATTTTCTTG	TCTTTAAAAT	TATCTAATCT	TTCCATTTTT	TCCCTATTCC	AAGTCAATT	300
GCTTCTCTAG	CCTCATTTCC	TAGCTCTTAT	CTACTATTAG	TAAGTGCTT	TTTCCCTAAA	360
AGGGAAAACA	GGAGAGAGA	ATGGCACACA	AAACAAACAT	TTTATATTCA	TATTTCTACC	420
TACGTTAATA	AAATAGCATT	TTGTGAAGCC	AGCTAAAAG	AAGGCTTAGA	TCCTTTATG	480
TCCATTTAG	TCACTAAACG	ATATCNAAG	TGCCAGAATG	CAAAGGTTT	GTGAACATT	540
ATTCAAAAGC	TAATATAAGA	TATTCACAT	ACTCATCTT	CTG		583

(2) INFORMATION FOR SEQ ID NO:204:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 589 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:204:

TTTTTTTTNT	TTTTTTTTTT	TTTTTNCTC	TTCTTTTTTT	TTGANAATGA	GGATCGAGTT	60
TTTCACTCTC	TAGATAGGGC	ATGAAGAAAA	CTCATCTTC	CAGCTTTAAA	ATAACAAATCA	120
AATCTCTTAT	GCTATATCAT	ATTTTAAGTT	AAACTAATGA	GTCACTGGCT	TATCTCTCC	180
TGAAGGAAAT	CTGTTCATTC	TTCTCATTCA	TATAGTTATA	TCAAGTACTA	CCTTGCATAT	240
TGAGAGGTTT	TTCTTCTCTA	TTTACACATA	TATTTCCATG	TGAATTGTA	TCAAACCTTT	300
ATTTTCATGC	AAACTAGAAA	ATAATGTNTT	CTTTTGCATA	AGAGAAGAGA	ACAATATNAG	360
CATTACAAA	CTGCTAAAT	TGTTTGTAA	GNTTATCCAT	TATAATTAGT	TNGGCAGGAG	420
CTAATACAAA	TCACATTTC	NGACNAGCAA	TAATAAAACT	GAAGTACCA	TTAAATATCC	480
AAATAATTA	AAGGAACATT	TTTACCTGG	GTATAATTAG	CTAATTCACT	TTACAAGCAT	540
TTATTNAGAA	TGAATTCA	TGTTATTATT	CCNTAGCCCA	ACACAATGG		589

(2) INFORMATION FOR SEQ ID NO:205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 545 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:205:

TTTTTNTTTT	TTTTTCAGT	ATAATCAGA	ACAATATTTA	TTTTTATATT	AAAATT	60
AGAAAAGTGC	CTTACATTTA	ATAAAAGTTT	GTTCCTCAAA	GTGATCAGAG	GAATTAGATA	120
TNGTCTTGAA	CACCAATATT	AATTGAGGA	AAATACACCA	AAATACATTA	AGTAAATTAT	180
TTAAGATCAT	AGAGCTTGTA	AGTAAAAGA	AAAATTGTA	CCTCAGAAC	TCTGAGCATT	240
AAAAATCCAC	TATTAGCAA	AAATTACTA	TGGACTTCTT	GCTTTAATT	TGTGATGAAT	300
ATGGGGTGTG	ACTGGTAAAC	CAACACATT	TGAAGGGATAC	ATTACTTAGT	GATAGATTCT	360
TATGTACTTT	GCTANATNAC	GTGGATATGA	GTGACAAGT	TTCTCTTCT	TCAATCTTT	420
AAGGGGCNGA	NGAAATGAGG	AAGAAAAGAA	AAGGATTACG	CATACTGTTC	TTTCTATNGG	480
AAGGATTAGA	TATGTTTCCT	TTGCCAATAT	TAaaaaAAATA	ATAATGTTA	CTACTAGTGA	540
AACCC						545

(2) INFORMATION FOR SEQ ID NO:206:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 487 base pairs

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:206:

TTTTTTTTTT	TTTTTAGTC	AAGTTCTNA	TTTTTATTAT	AATTAAAGTC	TTGGTCATTT	60
CATTTATTAG	CTCTGCAACT	TACATATTTA	AATTAAAGAA	ACGTTNTTAG	ACAACGTGNA	120
CAATTATAAA	ATGTAAGGTG	CCATTATTGA	GTANATATAT	TCCTCCAAGA	GTGGATGTGT	180
CCCTTCTCCC	ACCAACTAAT	GAANCAGCAA	CATTAGTTA	ATTTTATTAG	TAGATNATAC	240
ACTGCTGAA	ACGCTAATTTC	TCTTCTCCAT	CCCCATGTNG	ATATTGTGTA	TATGTGTGAG	300
TTGGTNAGAA	TGCATCANCA	ATCTNACAAT	CAACAGCAAG	ATGAAGCTAG	GCNTGGGCTT	360
TCGGTGAAAA	TAGACTGTGT	CTGTCTGAAT	CAAATGATCT	GACCTATCCT	CGGTGGCAAG	420
AACTCTTCGA	ACCGCTTCCT	CAAAGGCNGC	TGCCACATTT	GTGGCNTCTN	TTGCACTTGT	480
TTCAAAA						487

(2) INFORMATION FOR SEQ ID NO:207:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 332 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:207:

TGAATTGGCT	AAAAGACTGC	ATTTTTANAA	CTAGCAACTC	TTATTTCTTT	CCTTTAAAAAA	60
TACATAGCAT	AAAATCCAA	ATCCTATTAA	AAGACCTGAC	AGCTTGAGAA	GGTCACTACT	120
GCATTTATAG	GACCTTCTGG	TGGTTCTGCT	GTACNTTTG	AANTCTGACA	ATCCTTGANA	180
ATCTTGCAT	GCAGAGGAGG	TAAAAGGTAT	TGGATTTCA	CAGAGGAANA	ACACAGCGCA	240
AAAATGAAGG	GGCCAGGCTT	ACTGAGCTTG	TCCACTGGAG	GGCTCATGGG	TGGGACATGG	300
AAAAGAAGGC	AGCCTAGGCC	CTGGGGAGCC	CA			332

(2) INFORMATION FOR SEQ ID NO:208:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 524 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:208:

AGGGCGTGGT	GCGGAGGGCG	TTACTGTTT	GTCTCAGTAA	CAATAAATAC	AAAAAGACTG	60
GTTGTGTTC	GGCCCCATCC	AACCACGAAG	TTGATTTCTC	TTGTGTGCAG	AGTGACTGAT	120
TTTAAAGGAC	ATGGAGCTTG	TCACAAATGTC	ACAATGTCAC	AGTGTGAAGG	GCACACTCAC	180
TCCCGCGTGA	TTCACATTAA	GCAACCAACA	ATAGCTCATG	AGTCCATACT	TGTAAATACT	240
TTTGGCAGAA	TACTTNTGAA	AACTTGCAGA	TGATAACTAA	GATCCAAGAT	ATTTCCAAA	300
GTAAATAGAA	GTGGGTCTATA	ATATTAATTA	CCTGTTACAA	TCAGCTTCCA	TTTACAAGTC	360
ATGAGGCCAG	ACACTGACAT	CAAACAAAGC	CCACTTAGAC	TCCTCACCAC	CAGTCTGTCC	420
TGTCATCAGA	CAGGAGGCTG	TCACCTTGAC	CAAATTCTCA	CCAGTCAATC	ATCTATCCAA	480
AAACCATTAC	CTGATCCACT	TCCGGTAATG	CACCACCTTG	GTGA		524

(2) INFORMATION FOR SEQ ID NO:209:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:209:

GGGTGAGGAA ATCCAGAGTT GCCATGGAGA AAATTCCAGT GTCAGCATTC TTGCTCCTTG	60
TGGCCCTCTC CTACACTCTG GCCAGAGATA CCACAGTCAA ACCTGGAGCC AAAAAGGACA	120
CAAAGGACTC TCGACCCAAA CTGCCAGA CCCTCTCCA	159

(2) INFORMATION FOR SEQ ID NO:210:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 256 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:210:

ACTCCCTGGC AGACAAAGGC AGAGGAGAGA GCTCTGTTAG TTCTGTGTTG TTGAAC TGCC	60
ACTGAATTTC TTTCCACTTG GACTATTACA TGCCANTGGA GGGACTAATG GAAAAACGTA	120
TGGGGAGATT TTANCCAATT TANGTNTGTA AATGGGGAGA CTGGGGCAGG CGGGAGAGAT	180
TTGCAGGGTG NAAATGGGAN GGCTGGTTG TTANATGAAC AGGGACATAG GAGGTAGGCA	240
CCAGGATGCT AAATCA	256

(2) INFORMATION FOR SEQ ID NO:211:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 264 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:211:

ACATTGTTTT TTTGAGATAA AGCATTGAGA GAGCTCTCCT TAACGTGACA CAATGGAAGG	60
ACTGGAACAC ATACCCACAT CTTTGTCTG AGGGATAATT TTCTGATAAA GTCTTGCTGT	120
ATATTCAAGC ACATATGTTA TATATTATTAC AGTTCCATGT TTATAGCCTA GTTAAGGAGA	180
GGGGAGATAC ATTNCNGAAAG AGGACTGAAA GAAATACTCA AGTNGGAAAA CAGAAAAAAGA	240
AAAAAAGGAG CAAATGAGAA GCCT	264

(2) INFORMATION FOR SEQ ID NO:212:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 328 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:212:

ACCCAAAAAT CCAATGCTGA ATATTTGGCT TCATTATTCC CANATTCTTT GATTGTCAA	60
GGATTTAATG TTGCTCAGC TTGGGCACCTT CAGTAGGAC CTAAGGATGC CAGCCGGCAG	120
GTTTATATAT GCAGCAACAA TATTCAAGCG CGACAACAGG TTATTGAACT TGCCCAGCAG	180
TTNAATTTC TTCCCATTGA CTTGGGATCC TTATCATCAG CCAGAGAGAT TGAAAATTAA	240
CCCCCTACNAC TCTTACTCT CTGGANAGGG CCAGTGGTGG TAGCTATAAG CTTGGCCACA	300
TTTTTTTTTC CTTTATTCCCT TTGTCAGA	328

(2) INFORMATION FOR SEQ ID NO:213:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 250 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:213:

ACTTATGAGC AGAGCGACAT ATCCNAGTGT AGACTGAATA AACTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120
CATTATGCCA AAAGGAAATAT ACATTTCAAT TCTCCAAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTTT GCATGAACCT GCTGATAANC CATGTTAANA AACAAATATC TCTCTNACCT	240
TCTCATCGGT	250

(2) INFORMATION FOR SEQ ID NO:214:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 444 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:214:

ACCCAGAACAT CAATGCTGAA TATTTGGCTT CATTATTCCC AGATTCTTTG ATTGTCAAAG	60
GATTAAATGT TGTCTCAGCT TGGGCACCTTC AGTTAGGACC TAAGGATGCC AGCCGGCAGG	120
TTTATATATG CAGCAACAAAT ATTCAAGCGC GACAACAGGT TATTGAACTT GCCCGCCAGT	180
TGAATTCAT TCCCATTGAC TTGGGATCCT TATCATCAGC CANAGAGATT GAAAATTAC	240
CCCTACGACT CTTTACTCTC TGGAGAGGGC CAGTGGTGGT AGCTATAAGC TTGGCCACAT	300
TTTTTTTTCC TTTAATCCCT TGTCAAGAGAT CGCATTTCATC CATATGCTAN AAACCAACAG	360
AGTGACTTTT ACAAAATTCC TATAGANATT GTGAATAAAA CCTTACCTAT AGTTGCCATT	420
ACTTGCTCT CCCTAAATATAA CCTC	444

(2) INFORMATION FOR SEQ ID NO:215:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 366 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:215:

ACTTATGAGC AGAGCGACAT ATCCAAGTGT ANACTGAATA AACTGAATT CTCTCCAGTT	60
TAAAGCATTG CTCACTGAAG GGATAGAAGT GACTGCCAGG AGGGAAAGTA AGCCAAGGCT	120

CATTATGCCA AAGGANATAT ACATTTCAAT TCTCCAACT TCTTCCTCAT TCCAAGAGTT	180
TTCAATATTT GCATGAACCT GCTGATAAGC CATGTTGAGA AACAAATATC TCTCTGACCT	240
TCTCATCGGT AAGCAGAGGC TGTAGGCAAC ATGGACCATA GCGAANAAAA AACTTAGTAA	300
TCCAAGCTGT TTTCTACACT GTAACCAGGT TTCCAACCAA GGTGGAAATC TCCTATACTT	360
GGTGCC	366

(2) INFORMATION FOR SEQ ID NO:216:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:216:

CTGTATAAAC AGAACTCCAC TGCAANGAGGG AGGGCCGGGC CAGGAGAATC TCCGCTTGTC	60
CAAGACAGGG GCCTAAGGAG GGTCTCCACA CTGCTNNNTAA GGGCTNTTNC ATTTTTTTAT	120
TAATAAAAAG TNNAAAAGGC CTCTTCTCAA CTTTTTCCC TTNGGCTGGA AAATTTAAAA	180
ATCAAAAATT TCCTNAAGTT NTCAAGCTAT CATATATACT NTATCCTGAA AAAGCAACAT	240
AATTCTTCCT TCCCTCCTTT	260

(2) INFORMATION FOR SEQ ID NO:217:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 262 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:217:

ACCTACGTGG GTAAGTTAN AAATGTTATA ATTCAGGAA NAGGAACGCA TATAATTGTA	60
TCTTGCTAT AATTTCTAT TTTAATAAGG AAATAGCAA TTGGGGTGGG GGGAAATGTAG	120
GGCATTCTAC AGTTTGAGCA AAATGCAATT AAATGTGGAA GGACAGCACT GAAAAATTAA	180
ATGAATAATC TGTATGATTA TATGTCTCTA GAGTAGATT ATAATTAGCC ACTTACCTA	240
ATATCCTTCA TGCTTGAAA GT	262

(2) INFORMATION FOR SEQ ID NO:218:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 205 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:218:

ACCAAGGTGG TGCATTACCG GAANTGGATC AANGACACCA TCGTGGCAA CCCCTGAGCA	60
CCCTTATCAA CTCCCTTTG TAGTAAACTT GGAACCTTGG AAATGACCAG GCCAAGACTC	120
AGGCCTCCCC AGTTCTACTG ACCTTTGTCC TTANGNTNA NGTCCAGGGT TGCTAGGAAA	180
ANAAAATCAGC AGACACAGGT GTAAA	205

(2) INFORMATION FOR SEQ ID NO:219:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 114 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:219:

TACTGTTTG TCTCAGTAAC AATAAAATACA AAAAGACTGG TTGTGTTCCG GCCCCATCCA	60
ACCACGAAGT TGATTCTCT TGTGTGCAGA GTGACTGATT TAAAGGACA TGGA	114

(2) INFORMATION FOR SEQ ID NO:220:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 93 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:220:

ACTAGCCAGC ACAAAAGGCA GGGTAGCCTG ATTGCTTTC TGCTCTTAC ATTTCTTTA	60
AAATAAGCAT TTAGTGCTCA GTCCCCTACTG AGT	93

(2) INFORMATION FOR SEQ ID NO:221:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 167 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:221:

ACTANGTGCA GGTGCGCACA AATATTGTC GATATTCCCT TCATCTTGGAA TTCCATGAGG	60
TCTTTGCC AGCCTGTGGC TCTACTGTAG TAAGTTCTG CTGATGAGGA GCCAGNATGC	120
CCCCCACTAC CTTCCCTGAC GCTCCCCANA AATCACCAA CCTCTGT	167

(2) INFORMATION FOR SEQ ID NO:222:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 351 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:222:

AGGGCGTGGT GCGGAGGGCG GTACTGACCT CATTAGTAGG AGGATGCATT CTGGCACCC	60
GTTCTTCACC TGTCCCCCAA TCCTTAAAG GCCATACTGC ATAAAGTCAA CAACAGATAA	120
ATGTTTGCTG AATTAAAGGA TGGATGAAAA AAATTAATAA TGAATTTTG CATAATCAA	180
TTTTCTCTT TATATTCTA GAAGAAGTTT CTTTGAGCCT ATTAGATCCC GGGAAATCTT	240
TAGGTGAGCA TGATTAGAGA GCTTGTAGGT TGCTTTACA TATATCTGGC ATATTTGAGT	300

CTCGTATCAA AACAAATAGAT TGGTAAAGGT GGTATTATTG TATTGATAAG T 351

(2) INFORMATION FOR SEQ ID NO:223

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 383 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:223:

AAAACAAACA AACAAAAAAA ACAATTCTTC ATTCAAGAAA ATTATCTTAG GGACTGATAT	60
TGGTAATTAT GGTCAATTAA ATWRTRTTK GTGGCATTT CTTACATTGT CTTGACAAGA	120
TTAAAATGTC TGTGCCAAA TTTGTATTT TATTTGGAGA CTTCTTATCA AAAGTAATGC	180
TGCCAAAGGA AGTCTAAGGA ATTAGTAGTG TTCCCMTCAC TTGTTGGAG TGTGCTATT	240
TAAAAGATTT TGATTTCTG GAATGACAAT TATATTTAA CTTTGGTGGG GGAAANAGTT	300
ATAGGACCAC AGTCTTCACT TCTGATACTT GTAAATTAAT CTTTATTGC ACTTGTGG	360
ACCATTAAGC TATAIGTTA AAA	383

(2) INFORMATION FOR SEQ ID NO:224

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 320 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:224

CCCCTGAAGG CTTCTTGTAA GAAAATAGTA CAGTTACAAC CAATAGGAAC AACAAAAAGA	60
AAAAGTTGT GACATTGTAG TAGGGAGTGT GTACCCCTTA CTCCCCATCA AAAAAAAAT	120
GGATACATGG TTAAAGGATA RAAGGGCAAT ATTTTATCAT ATGTTCTAAA AGAGAAGGAA	180
GAGAAAATAC TACTTCTCR AAATGGAAGC CCTTAAAGGT GCTTGATAC TGAAGGACAC	240
AAATGTGGCC GTCCATCCTC CTTTARAGTT GCATGACTTG GACACGGTAA CTGTTGCAGT	300
TTTARACTCM GCATTGTGAC	320

CLAIMS

1. A polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220, 222-224, the complements of said nucleotide sequences and variants of said nucleotide sequences.

2. A DNA molecule comprising a nucleotide sequence encoding the polypeptide of claim 1.

3. A DNA molecule having a sequence provided in SEQ ID NOS: 2, 3, 8-29, 41-45, 47-52, 54-65, 70, 73-74, 79, 81, 87, 90, 92, 93, 97, 103, 104, 107, 109-111, 115-160, 171, 173-175, 177, 181, 188, 191, 193, 194, 198, 203, 204, 207, 209-211, 220 and 222-224.

4. An expression vector comprising the DNA molecule of claims 2 or 3.

5. A host cell transformed with the expression vector of claim 4.

6. The host cell of claim 5 wherein the host cell is selected from the group consisting of *E. coli*, yeast and mammalian cell lines.

7. A pharmaceutical composition comprising the polypeptide of claim 1 and a physiologically acceptable carrier.

8. A vaccine comprising the polypeptide of claim 1 and a non-specific immune response enhancer.

9. The vaccine of claim 8 wherein the non-specific immune response enhancer is an adjuvant.

10. A vaccine comprising the DNA molecule of claims 2 or 3 and a non-specific immune response enhancer.

11. The vaccine of claim 10 wherein the non-specific immune response enhancer is an adjuvant.

12. A pharmaceutical composition for the treatment of prostate cancer comprising a polypeptide and a physiologically acceptable carrier, the polypeptide comprising an immunogenic portion of a prostate protein or of a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219 and 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

13. A vaccine for the treatment of prostate cancer comprising a polypeptide and a non-specific immune response enhancer, said polypeptide comprising an immunogenic portion of a prostate protein or a variant thereof, wherein said protein comprises an amino acid sequence encoded by a DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences

14. The vaccine of claim 13 wherein the non-specific immune response enhancer is an adjuvant.

15. A vaccine for the treatment of prostate cancer comprising a DNA molecule and a non-specific immune response enhancer, the DNA molecule having a sequence selected from the group consisting of nucleotide sequences recited in SEQ ID Nos: 5-7, 30-40, 46, 53, 66-69, 71, 72, 75-78, 80, 82-86, 88, 89, 91, 94-96, 98-102, 105, 106, 161-170, 179, 180, 182-187, 189, 190, 192, 195-197, 199-202, 205, 206, 208, 212-219, 221, the complements of said nucleotide sequences and variants of said nucleotide sequences.

16. The vaccine of claim 15 wherein the non-specific immune response enhancer is an adjuvant.

17. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claims 7 or 12.

18. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of any one of claims 8, 10, 13 or 15.

19. A fusion protein comprising two or more polypeptides according to claim 1.

20. A fusion protein comprising a polypeptide according to claim 1 and a known prostate antigen.

21. A pharmaceutical composition comprising a fusion protein according to any one of claims 19-20 and a physiologically acceptable carrier.

22. A vaccine comprising a fusion protein according to any one of claims 19-20 and a non-specific immune response enhancer.

23. The vaccine of claim 22 wherein the non-specific immune response enhancer is an adjuvant.

24. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the pharmaceutical composition of claim 21.

25. A method for inhibiting the development of prostate cancer in a patient, comprising administering to the patient an effective amount of the vaccine of claim 22.